

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 10:10:05 ; Search time 1326 Seconds

(without alignments)
167.217 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217

Sequence: 1 MAAAMAATTMTTKNNRASLV.....TETGAGGQAAPKSGNDPR 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1906.5	86.0	396	2	Q6E5A5
2	1549	69.9	425	2	Q6Z782
3	1401.5	63.2	436	1	BTI_MALZE
4	1318.5	59.5	419	2	Q65XJ8
5	1192	53.8	415	2	Q65XJ8
6	1082.5	48.8	385	2	Q9ZNY4
7	1041	47.0	392	2	Q9ZNY4
8	580	26.2	238	2	Q8W008
9	563.5	25.4	385	2	Q6YZW6
10	561.5	25.3	346	2	Q8LJF38
11	561.5	25.3	348	2	Q9LJX5
12	464	20.9	318	2	Q8R0Y8
13	463	20.9	338	2	Q7RXJ3
14	462.5	20.9	352	2	Q04619
15	461	20.8	355	2	Q6E583
16	457	20.6	458	2	Q705K4
17	457	20.6	477	2	Q6NWX1
18	457	20.6	477	2	Q6NWX1
19	454	20.5	475	2	Q18757
20	452.5	20.4	515	2	Q69X19
21	450	20.3	318	2	Q86VD7
22	450	20.3	467	2	Q6GQ51
23	450	20.3	475	2	Q7TFC2
24	450	20.3	475	2	Q8BMD8
25	448	20.2	384	2	Q96N04
26	448	20.2	468	2	Q705K3
27	446.5	20.1	322	2	Q9TUS2
28	442	19.9	477	2	Q66L49
29	440.5	19.9	524	2	Q7PNW8
30	437	19.7	326	2	Q12251
31	436	19.7	476	2	Q6Z790

32	435	19.6	316	2	Q9N137	Q9N137 trichomonas
33	432	19.5	338	2	Q6C3A2	Q6C3A2 yarrowia 11
34	428.5	19.3	365	2	Q8W4M2	Q8W4M2 arabidopsis
35	428.5	19.3	473	2	Q7R0U6	Q7R0U6 xenopus lae
36	427.5	19.3	487	2	Q9T143	Q9T143 arabidopsis
37	427.5	19.3	501	2	Q6NWX8	Q6NWX8 mus musc
38	427.5	19.3	514	2	Q8JZT8	Q8JZT8 mus musc
39	427.5	19.3	515	2	Q80T78	Q80T78 mus musc
40	426.5	19.2	469	2	Q8K3P6	Q8K3P6 rattus norv
41	426	19.2	305	2	Q86DE1	Q86DE1 trichomonas
42	425.5	19.2	337	2	Q817R0	Q817R0 arabidopsis
43	425.5	19.2	367	2	Q6Z763	Q6Z763 arabidopsis
44	425.5	19.2	337	2	Q8VBT4	Q8VBT4 mus musc
45	425.5	19.2	502	2	Q8BH0	Q8BH0 m mus musc

ALIGNMENTS

RESULT 1

ID	Q6E5A5	PRELIMINARY	PRT	396 AA.
AC	Q6E5A5			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Plastidial ADP-glucose transporter.			
OS	Hordeum vulgare var. distichum (Two-rowed barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxID=112509;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15299120; DOI=10.1104/pp.104.045203;			
RA	Patron N.J., Greber B., Fahy B.F., Laurie D.A., Parker M.L.,			
RA	Denyer K.;			
RT	"The Iyres Mutations of Barley Reveal the Nature and Importance of			
RT	Plastidial ADP-Glc Transporters for Starch Synthesis in Cereal			
RT	Endosperm.";			
RL	Plant Physiol. 135:2088-2097(2004).			
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.			
DR	EMBL; AY560327; AAT12275.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005743; C:mitochondrial inner membrane; IEA.			
DR	GO; GO:0005739; C:mitochondrion; IEA.			
DR	GO; GO:0005488; F:binding; IEA.			
DR	GO; GO:0005351; F:sugar porter activity; IEA.			
DR	GO; GO:0006839; F:mitochondrial transport; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR001993; Mitoch_carrier.			
DR	InterPro; IPR002067; Mit_carrier.			
DR	InterPro; IPR002030; Mit_uncoupling.			
DR	Pfam; PF00153; Mito_carr; 3.			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	PRINTS; PR00784; MITOCOUPLING.			
DR	PROSITE; PS50920; SOLCAR; 3.			
KW	Sugar transporter; Transmembrane; Transport.			
SEQ	SEQUENCE 396 AA; 42436 MW; 37EE334FDF24FB8D CRC64;			
Query Match	86.0%; Score 1906.5; DB 2; Length 396;			
Best Local Similarity	92.3%; Pred. No. 3.1e-136;			
Matches	373; Conservative 7; Mismatches 15; Indels 9; Gaps 1;			
QY	1 MAAAMAATTMTTKNNRASLVNDKKMLRPVEVAFPWSSQPSRSLDFPRRALFASVGL 60			
DB	1 MAAAMAATTMTTKNNRASLVNDKKMLRPVEVAFPWSSQPSRSLDFPRRALFASVGL 60			
QY	61 SLSHGAPVAAREHDKAPADVDVAHQLAAGEAGYQKAKKAKKQOLSLRKVRVKN 120			
DB	61 SLSHGAPVAAREHDKAPADVDVAHQLAAGEAGYQKAKKAKKQOLSLRKVRVKN 120			
QY	121 PHLRLVSGALAGAVSRFVAPLETIRTHLMVSGSGADSMAGVFRIMRTGMPGLFRGN 180			
DB	121 PHLRLVSGALAGAVSRFVAPLETIRTHLMVSGSGADSMAGVFRIMRTGMPGLFRGN 180			

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Db 112 PHLRRLVSGAIGAVSRFTVAPLETIRTHLMVSSGADSMGQVWRIMRTGEMGLFRGN 171
Qy 181 AAVNVLRAVPSKAIHFHYTDRAKKYLTPEAGEPAPVPIPTPLVAGALGVASTLCTYEMEL 240
Db 172 AAVNVLRAVPSKAIHFHYTDRAKKYLTPEAGEPAPVPIPTPLVAGALGVASTLCTYEMEL 231
Qy 241 VKRRLTEKQVYDNLHAFVKIVRDEGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Db 232 VKRRLTEKQVYDNLHAFVKIVRDEGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 291
Qy 301 PRAASKEEVGNVPTLLIGSAGALASTATPEPLEVARKOMQVAGVGRQYKLVHMYCI 360
Db 292 PRAASKEEVGNVPTLLIGSAGALASTATPEPLEVARKOMQVAGVGRQYKLVHMYCI 351
Qy 361 LEKEGTAGLYRGLGSPSCIKLMPAAGISFMCYEACKILVDEKED 404
Db 352 LNREGAAGLYRGLGSPSCIKLMPAAGISFMCYEACKILINNOE 395

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RESULT 2

062782 PRELIMINARY; PRT; 425 AA.

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ID 062782
AC 062782;
DT 05-JUL-2004 (TREMBlrel, 27, Created)
DT 05-JUL-2004 (TREMBlrel, 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel, 27, Last annotation update)
DE Putative Brittle-1 protein, chloroplast.
GN Name=P0419A09.38; Synonyms=O01135_F06.4;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL: AP004669; BAD15863.1; -.
DR EMBL: AP004045; BAD15497.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005743; C: mitochondrial inner membrane; IEA.
DR GO: GO:0005739; C: mitochondrial inner membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0006839; P: mitochondrial transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR; 3.
KW Transmembrane; Transport.
SQ
SEQUENCE 425 AA; 45363 MW; 2088B20220BF2CA1 CRC64;

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Query Match 69.9%; Score 1549; DB 2; Length 425;

Best Local Similarity 75.2%; Pred. No. 4.5e-109; Indels 34; Gaps 8;

Matches 327; Conservative 21; Mismatches 53;

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Qy 1 MAAMAATTWTKNNR-----ASLVMDKKNNLLRPVEVAPWWS-----QPSRSIDFP 50
Db 1 MAAMAATTWTKNNR-----ASLVMDKKNNLLRPVEVAPWWS-----QPSRSIDFP 57
Qy 51 RRA---LFAVGLSHGAPPAVAREHDKARPADVVAHOLA--AGEAGVQKAK-K 103
Db 58 RRTAAPPLFAVGLSHGAPPAVAREHDKARPADVVAHOLA--AGEAGVQKAK-K 108

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Qy 104 AKKOQLSRKRVKIGNPHLRVSGAIGAVSRFTVAPLETIRTHLMVSSGADSMAGV 163
Db 109 GGGGLSLRKRVKIGNPHLRVSGAIGAVSRFTVAPLETIRTHLMVSSGADSMAGV 168
Qy 164 FRIMRTGEGPGLFRGNANVTLRAVPSKAIHFHYTDRAKKYLTPEAGEPAPVPIPTPLV 223
Db 169 FRIMRTGEGPGLFRGNANVTLRAVPSKAIHFHYTDRAKKYLTPEAGEPAPVPIPTPLV 228
Qy 224 GALAGVASTLCTYEMELVTRLTIEKQVYDNLHAFVKIVRDEGPGLYRGLAPSLIGVY 283
Db 229 GALAGVASTLCTYEMELVTRLTIEKQVYDNLHAFVKIVRDEGPGLYRGLAPSLIGVY 288
Qy 284 PYAANFYAVETLRGVYRRAASKEEVGNVPTLLIGSAGALASTATPEPLEVARKOMQV 343
Db 289 PYAATFYAVETLRRLYRATGRADVGPATLLIGSAGALASTATPEPLEVARKOMQV 348
Qy 344 VGGROYKLVHMYCILEKEGTAGLYRGLGSPSCIKLMPAAGISFMCYEACKILVDEK 403
Db 349 VGGROYKLVHMYCILEKEGTAGLYRGLGSPSCIKLMPAAGISFMCYEACKILVDEK 407
Qy 404 DGAAREPQETENGQ 418
Db 408 ---AAPELAECAE 418

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RESULT 3

BT1_MAIZE STANDARD; PRT; 436 AA.

ID BT1_MAIZE

AC P29518;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Brittle-1 protein, chloroplast precursor.

GN Name=BT1.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=93005685; PubMed=1668652;

RA Sullivan T.D., Strelow L.I., Illingworth C.A., Phillips R.L.,

RA Nelson O.E., Jr.;

RT "Analysis of maize brittle-1 alleles and a defective suppressor-

mutator-induced mutable allele.";

RL Plant Cell 3:137-1348(1991).

CC -1- FUNCTION: Could play a role in amyloplast membrane transport.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast inner

membrane; amyloplast inner membrane (Potential).

CC -1- TISSUE SPECIFICITY: Endosperm of developing kernels.

CC -1- SIMILARITY: Contains 3 Solcar repeats.

CC -1- SIMILARITY: Contains 3 Solcar repeats.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

at the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

CC EMBL: M79333; AAA3438.1; -.

DR PIR: J01459; J01459.

DR MaizeDB: 47578; -.

DR InterPro: IPR002067; Mlt_carrier.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; Mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PROSITE: PS50920; SOLCAR; 3.

DR Amyloplast; Chloroplast; Inner membrane; Repeat; Transit peptide;

KW Transmembrane; Transport.

FT TRANSIT 1 75 Chloroplast (Potential).

FT CHAIN 76 436 Brittle-1 protein.
 FT TRANSMEM 229 247 Potential.
 FT TRANSMEM 327 347 Potential.
 FT REPEAT 132 216 Solcar 1.
 FT REPEAT 227 311 Solcar 2.
 FT REPEAT 324 412 Solcar 3.
 SO SEQUENCE 436 AA; 46627 MW; 9600C05F603E9DAB CRC64;

Query Match 63.2%; Score 1401.5; DB 1; Length 436;
 Best Local Similarity 65.4%; Pred. No. 7,1e-98;
 Matches 291; Conservative 46; Mismatches 69; Indels 39; Gaps 9;

QY 1 MAAAATATMTYKNNRASIYMDKKNMLRPVEVAFPMSQ--PESRSLDFPRRALFASVG 59
 DB 1 MAATTAATVTTMTYRS-----KESMSLQVPAVAFPMKPRGCKTGLEFPARAMFASVG 52
 QY 60 LSLSHGAPP--VARHDKG-ARPAD--DYAHQLAAGENGAVOKAKKAKKQQLSLRV 114
 DB 53 LNVCGVPAGRDPREDPKVVPAADNCIDIASLAPPPGSRPPGRRGRGSEEEAEGRH 112
 QY 115 RVKIG-----NPHLRVLSGATAGAVSRFTVAPLETIRTHLMVSGSGADSM 160
 DB 113 EBAAGASSEPEEGQOROPAPARLVSGAAGAVSRFTVAPLETIRTHLMVSGIGVSM 172
 QY 161 AGVFPMIRTEGMPGLFRGNANVNLVAPSKAIEHTYDTAKKYLTPKAGEPAKPIPTP 220
 DB 173 AGVFPMIQNEGTMTLFRGNANVNLVAPSKAIEHTYDTAKKYLTPKAGEPAKPIPTP 232
 QY 221 LVAGALAGVASTLCTYPMELVTRLTTEKVDYDNLHAFVKIVDEGPELYRGLAPSLI 280
 DB 223 LVAGALAGVASTLCTYPMELVTRLTTEKVDYDNLHAFVKILRDEGPELYRGLAPSLI 292
 QY 291 GVPFPAANFYAYETLRGYRRASGK---EYGNVPTLLIGSAAAIASSTAFPLEVARK 337
 DB 293 GVPFPAACNFAYETLRKLYRRATRRPADVPVATLLIGSAAAIASSTAFPLEVARK 352
 QY 338 QMVGAVGGRQYKYNVLAHMYCIIEKEGTAGLYRGSPCICLMPAAGISPMCYEACKKI 397
 DB 353 QMVGAVGGRQYKYNVLAHMYCIIEKEGTAGLYRGSPCICLMPAAGISPMCYEACKKI 412
 QY 398 LVDEKEDGAAAPOEETETGAGGQ 422
 DB 413 LVDEKEDGAAAPOEETETGAGGQ 429

RESULT 4

Q69XJ8 PRELIMINARY; PRT; 419 AA.

AC Q69XJ8
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Putative mitochondrial energy transfer protein.
 GN Name=P0486H12.22;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaristaceae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.,
 RT "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 6, PAC
 RT clone: P0486H12.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL; AP003615; BAD3459.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; Mitoc_carri_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUOCOUPLING.
 DR PROSITE; PS50920; SOLCAR; 3.
 KW Transmembrane; Transport.
 SO SEQUENCE 419 AA; 45382 MW; AAA94E8CAD32BBAF CRC64;

Query Match 59.5%; Score 1318.5; DB 2; Length 419;
 Best Local Similarity 64.6%; Pred. No. 1.3e-91;
 Matches 270; Conservative 47; Mismatches 74; Indels 27; Gaps 7;

QY 10 MTKNNRASIYMDKKNMLRPVEVAFPMSQPE---SRSLD---FPRRALFASVGLSL 62
 DB 4 MSKSKNSVLTIEKQGSVPQLPRLRPMDLHEDKGSLSLHGSASPHGGLFASVGLVY 63
 QY 63 SHGAPPVA---REHDKARPADDVHQLAA-----GEAGVQAKAKKAKK 106
 DB 64 STAAVAVAPSPAEHDFKTPADHCKIKYSSAAGYGVPTGEASVNEEBEVDGKAVKAKK 123
 QY 107 QQLSLRKRVKIGNPHLRVLSGAIAGVSRFTVAPLETIRTHLMVSGSGADSMAGVFR 166
 DB 124 RGL---KIKIKIGNHLRLVLSGAVASRTCPVAPLETIRTHLMVSGSNG-DSMTEVFQS 179
 QY 167 IMRTGEGPGLFRGNANVNLVAPSKAIEHTYDTAKKYLTPKAGEPAKPIPTPLVAGAL 226
 DB 180 IMRTGEGPGLFRGNANVNLVAPSKAIEHTYDTAKKYLTPKAGEPAKPIPTPLVAGAL 239
 QY 227 AGVASTLCTYPMELVTRLTTEKVDYDNLHAFVKIVDEGPELYRGLAPSLI 286
 DB 240 AGVASTLCTYPMELVTRLTTEKVDYDNLHAFVKILRDEGPELYRGLAPSLI 299
 QY 287 AANFYAYETLRGYRRASGKEEVNPTLLIGSAAAIASSTAFPLEVARKQMGAVG 346
 DB 300 ATNYVAYDTLKLKYKTFQOEISNATLLIGSAAAIASSTAFPLEVARKQMGAVG 359
 QY 347 RQYKYNVLAHMYCIIEKEGTAGLYRGSPCICLMPAAGISPMCYEACKKI 404
 DB 360 RQYKYNVLAHMYCIIEKEGTAGLYRGSPCICLMPAAGISPMCYEACKKI 417

RESULT 5

Q65XR7 PRELIMINARY; PRT; 415 AA.

AC Q65XR7
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Putative adenylate translocator (Brittle-1) protein.
 GN Name=P0685E10.12;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaristaceae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Heiao S.-H.,
 RA Heing J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.,
 RT "Oryza sativa PAC P0685E10 genomic sequence."
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chow T.-Y.,
 RA Subtilted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC087553; AAU44334.1; -;
 SO SEQUENCE 415 AA; 44028 MW; 3B7A32081CBF1BE6 CRC64;

Query Match 53.8%; Score 1192; DB 2; Length 415;
 Best Local Similarity 65.3%; Pred. No. 5.2e-82;
 Matches 235; Conservative 47; Mismatches 72; Indels 6; Gaps 2;

50 PRRLFFASVGL-----SLSHGAPPVAREHDKAR-PADVAHQALAAAEAGVQKAKKA 104
 57 PASGLFASVGVGPATSSSPDPADGDPYAKYVSPSEIEHMLPGOSVEVELEMEKKKN 116
 105 KKQOLSTRKVRKVGKGNHRLVSGATAGAVSRTEVPLETRTHLVWSSGADSMGVF 164
 117 KKTKNFKFKIKIKGNHRLKSLSGAGAVSRVAPLETIRKTHLVWSSGADSMGVF 175
 165 RMIWTEGMPGLFRGNVNVTLRVAPSKAIEHFTYDTAKKYLTPRAGSPAKVPIPTPLVAG 224
 176 QSIKHGWTGLFRGNFVNIVRVAPSKAIEHFTYDTAKKYLTPRAGSPAKVPIPTPLVAG 235
 225 ALGAVASTCTYPPELVYKTRITKDYNDILHAFVKIIVDEGEGELYRGLAPSLGV 284
 236 AFAGVSTCTYPLELTKRITLIRGVYDNFLHVLVIREEGTELYRGLTPSLGV 295
 285 YAAAFAYETLRGVRRASKEEVNPTLLISAGATASTPTPLVARKOMGVAV 344
 296 YAAITNPAITDLKKAAYKMEFTNIGVPTLLISAGATASTPTPLVARKOMGVAV 355
 345 GGRVYKVVHLYAMCYCILEKGTAGLYRGLSPSCIKLMPAAGISPMCYEACKILVDEKED 404
 356 GGRVYKVVHLYAMCYCILEKGTAGLYRGLSPSCIKLMPAAGISPMCYEACKILVDEKED 415

RESULT 6
 Q9ZNY4 PRELIMINARY; PRT; 385 AA.

AC Q9ZNY4
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
 DE Mitochondrial energy transfer protein precursor.
 GN Name=britlet;
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN
 RP SEQUENCE FROM N.A.
 RA Rink U.A., Riesenmeier J.W., Willmitzer L.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rink U.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL; X98474; CAA67107.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0006410; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; MLC_carrier.
 DR Pfam; PF00153; Mito_cartr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PSS0920; SOLCAR; 3.
 KW signal; Transmembrane; Transport.
 FT SIGNAL 1 44 Potential.
 FT CHAIN 45 385 Potential.
 SQ SEQUENCE 385 AA; 41232 MW; 88716118792C0B84 CRC64;

Query Match 48.8%; Score 1082.5; DB 2; Length 385;
 Best Local Similarity 58.7%; Pred. No. 9.6e-74;
 Matches 222; Conservative 56; Mismatches 85; Indels 13; Gaps 5;

38 WSSQPSRSIDFPRALFASV-----GLSLSHGAPPVAREHDKAR-PADVAHQALAA 90

9 WGSNGVSKIQTFVLVLDLFAVGVGMGCVSSPNSSDSRDENGFKLPSYDLCMKYLSF 68
 91 GE-----AGVQKAKKAKKQOOLSTRKVRKVGKGNHRLVSGATAGAVSRTEVPLETT 146
 69 SEGFKLVNGEESGVYKKEKKKGL-KIKLVSNPRLKRLISATIGALSRTVAALGTT 127
 147 RTHLVWSSGADSMAGVFPFIMNTEGMPGLFRGNAVNLRVAPSKAIEHFTYDTAKKYL 206
 128 RTHLVWSSG-HSSTEVFNSIMKTEGWTGLFRGNFVNIVRVAPSKAIEHFTYDTAKKYL 186
 207 PEGGEPAKPIPTPLVAGALAGVASTCTYPPELVYKTRITKDYNDILHAFVKIIVRDE 266
 187 SKPEGOSKPIPTPLVAGACAGVSTLLYPLELVTRITLIRGVYDNFLHVLVIREEGTE 246
 267 GPGLRGLAPSLIGVFPYAAAFAYETLRGVRRASKEEVNPTLLISAGATASTPTPLV 326
 247 GPALRYGLTPSYTGVIPYAAAFAYETLRGVRRASKEEVNPTLLISAGATASTPTPLV 306
 327 TATFPLEVARKOMGVAGVGRVYKVVHLYAMCYCILEKGTAGLYRGLSPSCIKLMPAAGI 386
 307 TATFPLEVARKOMGVAGVGRVYKVVHLYAMCYCILEKGTAGLYRGLSPSCIKLMPAAGI 366
 387 SPMCYEACKILVDEKED 404
 367 SPMCYEACKILVDEKED 384

RESULT 7
 Q9SU1 PRELIMINARY; PRT; 392 AA.

AC Q9SU1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Aduy1ace translocator (Bt1tle-1)-like protein
 DE (A7432400/F8B4_100).
 GN Name=F8B4_100; Synonyms=AT432400;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N.A., Ardiles W., Buyschaert C., Daseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarejo R., Gieles J., Van Montagu M., Hohensei J., Mewes H.W.,
 RA Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N.A., Ardiles W., Buyschaert C., Daseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarejo R., Gieles J., Van Montagu M., Hohensei J., Mewes H.W.,
 RA Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
 RA Carinci P., Chang B., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;


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RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE:22088475; PubMed:12093376;
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldman K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [7]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Shlun P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Caminici P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamuya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the EMBL/GenBank/DBJ carrier family.
DR EMBL, AL034567; CAA23567.1; -
DR EMBL, AL161581; CAB79957.1; -
DR EMBL, AY074831; AAL69529.1; -
DR EMBL, AY084938; AAM61499.1; -
DR EMBL, AF372944; AAK50084.1; -
DR PIR, T05350; T05350.
DR GO, GO:0016021; C:integral to membrane; IEA.
DR GO, GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO, GO:0005488; F:binding; IEA.
DR GO, GO:0006810; F:transport; IEA.
DR InterPro, IPR001993; Mitoch carrier.
DR InterPro, IPR002067; Mitc carrier.
DR Pfam, PF00153; Mito carri. 3.
DR PRINTS, PR00926; MITOCARRIER.
DR PROSITE, PS50920; SOLCAR; 3.
KM Transmembrane; Transport.
SQ SEQUENCE 392 AA; 42571 MW; 556269D8C67640C2 CRC64;

Query Match
Best Local Similarity 47.0%; Score 1041; DB 2; Length 392;
Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

QY 92 EAGVQKAKQAKKAKKQQLSLRKVRKIGNPHLRRLVSGAIGAVSRTEFVAPELIRTHLM 151
DB 83 EEEVNGEKRRKKKKGGU---KIKIANPSLRRLSGAVAGAVRTVAPELIRTHLM 139
QY 152 VGSSGADSMAGVFRNIMRTGEPGLRGNAVNVLVAPSKAIEHTFTDTAKKYLTPPAGE 211
DB 140 VG-SSGNSSTEVFSIMKHEGWTGFRGNLVAVIRVAPRAVELFVFETVKKLSPPGQ 198
QY 212 PAKVGIPTPLVAGALAGVASTCTCYPMELVKRRLTEKOVYNNLHAPFKYTRDGPDEL 271
DB 199 ESKITIPASLGLACAGVSQTLTLTPLELVKRLTIQKGVYIGIDAFIKITIRGPTFL 258
QY 272 YRGLAPSLIGVVPYAAANFYAYETLRGVRRASGEVNVPTLLIGSAGAIASTATFP 331
DB 259 YRGLAPSLIGVVPYAAATNFAYDLSRKAVRSFKQEKIGNITLLIGSLAGLSSTATFP 318
QY 332 LEVARKQMGVANGRGROYKRVNLHAMCYCLEKEGTAGLYRGLGSPCKIKMPAAGISPMCY 391
DB 319 LEVARKHMGVANGRGVVYKMLHALVTLLIEHGILGWYKGLGSPCKIKLVPAAGISPMCY 378
QY 392 EACKKIIVDEKED 404
DB 379 EACKKIILNNDE 391

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Q8W008
ID Q8W008 PRELIMINARY; PRT; 238 AA.
AC Q8W008;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Britle-1-like protein.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed endosperm;
RA Villand P., Kleczkowski L.A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY033629; AAK55487.1; -
SQ SEQUENCE 238 AA; 25508 MW; 6CAD5AF88236E43D CRC64;

Query Match
Best Local Similarity 26.2%; Score 580; DB 2; Length 238;
Matches 138; Conservative 14; Mismatches 67; Indels 28; Gaps 5;

QY 1 MAAAMAATTTMTYKNNRASIYMDKKWMLRPVEVAFPPSSQPSRSLDPPRALFASVGL 60
DB 1 MAAAMAATTTMTYKNNRASIYMDKKWMLRPVEVAFPPSSQPSRSLDPPRALFASVGL 60
QY 61 SLSHGAPVAREHDKARPADVAHQLAAGAGVQKQAKKAKKQQLSLRKVRKIGN 120
DB 61 SLSS-----HNGKARPADVFSHQLAAGAGVQKQAKKAKKHLGLRKVRKIGN 111
QY 121 PHLRVLVSGAIGAVSRFRVAPLELIRTHLMVSSGADSMAGVFRNIMRTGEP----- 174
DB 112 PHLRVLVSGAIGAVSKOFRG-----AAGDQDPDPDGKLRPLHGRGFVVDHAG 162
QY 175 GLFRGNAVNVLVAPSKAIE-HFTYDTAKKYLTPPAGE--BPAYPIPTPLVAGALAGVA 230
DB 163 GVARPLPRQKORLPRAAEQGHRTIHLHGGVEVPDGGRRSQKVPPIPLRVLAGALAGVA 222
QY 231 STLCTYP 237
DB 223 QPCAPIP 229

RESULT 9
Q6YZW6 PRELIMINARY; PRT; 385 AA.
ID Q6YZW6;
AC Q6YZW6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Putative mitochondrial energy transfer protein.
GN Name=QJ1003.A09.8; Synonyms=P0689E12.32;
OS Oryza sativa (Japanese cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Saeki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nippondare (GA3) genomic DNA, chromosome 8, BAC
RT clone:QJ1003.A09."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippondare (GA3) genomic DNA, chromosome 8, PAC
RT clone:P0689E12."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL, AP005509; BAD10433.1; -

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RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Iankiev P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Seltremkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Fishman D.,
 RA Kryscofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmant S.A.,
 RA DeSouza C.C., Glasse L., Obach M.J., Berglund J., Voelker R.,
 RA Yarden O., Flanagan M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Nivdag D.O., Alex L.A., Mannhaup G., Ebbole D.J., Preilag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.,
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
 RL Nature 0:0-0(2003).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX0100743; EAA27338.1; -.
 DR HSSP; P02722; 10KC.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002113; Aden tnslictor.
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; Mito_carr; 3.
 DR PRINTS; PR00927; ADPTRNSLCASE.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS50920; SOLCAR; 3.
 KM Hypothetical protein; Transmembrane; Transport.
 SQ SEQUENCE 338 AA; 36981 MW; 29982DA98ED2BA82 CRC64;

Query Match 20.9%; Score 463; DB 2; Length 338;
 Best Local Similarity 33.9%; Pred. No. 7.9e-27;
 Matches 104; Conservative 59; Mismatches 124; Indels 20; Gaps 7;

QY 115 RYVIGNPHRLRYVSGAAGVSTFVAPLETRTHLVGSSGAD----SNAQVFRWMT 170
 DB 29 RSNVOPSTVAFACGAGVAGVSRVVSPLERLITLVQVSSGRVAYLVSQKALAKWRE 88
 QY 171 EGMPLGRGAVNVVLRVAPSKAIEHPTDYAKKYLTPDEAGPAPKPIPTPLVAGALAGVA 230
 DB 89 EGMPLGRGAVNVVLRVAPSKAIEHPTDYAKKYLTPDEAGPAPKPIPTPLVAGALAGVA 230
 QY 231 STLCYPMELVKTRLTIKDYDNL-----LHAFYKIVADEG--PGEELYGLAPS 278
 DB 148 SVTFYVLDIVRRLISIQTASFAELGERPRMPCGMETLVVMYRTGEGFPA-LYRGIVPT 206
 QY 279 LIGVVPFAANFAYETLRGVYRRAAGKEVGNVPTLLISAGATASTATPFLVARKQ 338
 DB 207 VAGVAPVGNLFVWEYEHVR-QYTLTDEQNPASVRKLIAGVAVQCTTYPEDVLR 265
 QY 339 MOVGAVGR-QVKNVLAHAYCTLEKEGTAGLVGSGSCIKLMPAAGISFMCEACKKI 397
 DB 266 FQINTMSGMGYQKIGIDAVRIVTEGIGLYKGIYVNLKVAIPSMASMSLTYEVRDP 325
 QY 398 LVDEKED 404
 DB 326 LVGKPE 332

RESULT 14
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 ID 004619;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE A.IG002N01.16 protein (Putative carrier protein)
 DE (A14901100/F2N1_16).

GN Name=A.IG002N01.16; Synonyms=A14901100, A14901100;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 RX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Scheet P., Maggi L.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wash-U;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
 RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shin P.,
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai U., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai U., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stonelking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Meyer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA EC Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL; AF007269; AAB61037.1; -.
 DR EMBL; AY056343; AAL07192.1; -.
 DR EMBL; AF360168; AAK25878.1; -.
 DR EMBL; AL161491; CAB80919.1; -.
 DR EMBL; AF412085; AAL06538.1; -.
 DR PIR; T01729; T01729.
 DR HSSP; P02722; 10KC.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002113; Aden tnslictor.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; Mito_carr; 3.
 DR PRINTS; PR00927; ADPTRNSLCASE.

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OM protein - protein search, using SW model

Run on: May 25, 2005, 13:40:20 ; Search time 919 Seconds
(without alignments)
157.608 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2217	100.0	433	9	US-09-796-766-18
2	2217	100.0	433	15	US-10-659-199-18
3	1529	69.0	440	15	US-10-425-114-53253
4	1521.5	68.6	439	15	US-10-425-114-50902
5	1521.5	68.3	439	15	US-10-425-114-65995
6	1470.5	66.3	414	16	US-10-437-963-150460
7	1401.5	63.2	436	9	US-09-796-766-21
8	1401.5	63.2	436	15	US-10-659-199-21
9	1329.5	60.0	423	16	US-10-437-963-146611
10	1310	59.1	444	15	US-10-425-114-63026
11	1309	59.0	444	15	US-10-425-114-63935
12	1309	59.0	444	15	US-10-425-114-52078
13	1192	53.8	415	16	US-10-437-963-122416

14	1151.5	51.9	431	15	US-10-425-114-67044	Sequence 67044, A
15	1139.5	51.4	289	9	US-09-796-766-20	Sequence 20, Appl
16	1139.5	51.4	289	15	US-10-659-199-20	Sequence 20, Appl
17	1077	48.6	391	15	US-10-424-559-285116	Sequence 285116, A
18	1001	45.2	272	9	US-09-796-766-14	Sequence 14, Appl
19	1001	45.2	272	15	US-10-659-199-14	Sequence 14, Appl
20	792	35.7	273	15	US-10-424-559-265334	Sequence 265334, A
21	754.5	34.0	233	16	US-10-437-963-150461	Sequence 150461, A
22	740.5	33.4	231	16	US-10-437-963-150463	Sequence 150463, A
23	691	31.2	177	16	US-10-767-701-47449	Sequence 47449, A
24	595.5	26.9	337	16	US-10-437-963-118448	Sequence 118448, A
25	589.5	26.6	410	9	US-09-796-766-10	Sequence 10, Appl
26	589.5	26.6	410	15	US-10-659-199-10	Sequence 10, Appl
27	580.5	26.2	397	15	US-10-425-114-64610	Sequence 64610, A
28	574	25.9	375	16	US-10-767-701-43678	Sequence 43678, A
29	569	25.7	382	16	US-10-767-701-42759	Sequence 42759, A
30	565.5	25.5	378	15	US-10-424-559-240836	Sequence 240836, A
31	563.5	25.4	385	16	US-10-437-963-122906	Sequence 122906, A
32	502.5	22.7	267	15	US-10-424-559-241909	Sequence 241909, A
33	481	21.7	111	16	US-10-767-701-38030	Sequence 38030, A
34	474	21.4	345	15	US-10-424-559-221235	Sequence 221235, A
35	467.5	21.1	352	15	US-10-424-559-221242	Sequence 221242, A
36	466.5	21.0	391	15	US-10-425-114-56333	Sequence 56333, A
37	463	20.9	252	9	US-09-796-766-4	Sequence 4, Appl1
38	463	20.9	252	15	US-10-659-199-4	Sequence 4, Appl1
39	461	20.8	355	16	US-10-437-963-184488	Sequence 184488, A
40	459	20.7	109	9	US-09-796-766-16	Sequence 16, Appl1
41	459	20.7	109	15	US-10-659-199-16	Sequence 16, Appl1
42	458.5	20.7	413	15	US-10-425-114-55333	Sequence 55333, A
43	458.5	20.7	473	15	US-10-424-559-245081	Sequence 245081, A
44	457	20.6	477	9	US-09-777-921A-2	Sequence 2, Appl1
45	457	20.6	477	15	US-10-698-489-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-09-796-766-18
; Sequence 18, Application US/09796766
; Patent No. US20010047523A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Ratafski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Trillium aestivum
US-09-796-766-18

Query Match 100.0%; Score 2217; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.7e-193;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMAATTMTVKNRSLVMDKQWLLRPVEVAFPMSSQPSRSRLDPPRRALFASVGL 60
DB 1 MAAAMAATTMTVKNRSLVMDKQWLLRPVEVAFPMSSQPSRSRLDPPRRALFASVGL 60
QY 61 SLSHGAPVAREHDCARPADVAHQAALAAAGAGVQAKAKKAKQOGLRKVRKYN 120
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Db 61 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKORAKKAKKQOLSLRKVRXIGN 120
Qy 121 PHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGADSMAGVPRMTREMGPFGRN 180
Db 121 PHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGADSMAGVPRMTREMGPFGRN 180
Qy 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVP1PTPLVAGALAGVASTLCTYPMEL 240
Db 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVP1PTPLVAGALAGVASTLCTYPMEL 240
Qy 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Db 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Qy 301 RRASGKEEVGNVPTLLIGSAGAIASATATPPELVARKOMOVAGVGRQVYKNVLHAMYCI 360
Db 301 RRASGKEEVGNVPTLLIGSAGAIASATATPPELVARKOMOVAGVGRQVYKNVLHAMYCI 360
Qy 361 LEKEGTAGLYRGIGPSCIKLMPAAGISFMCYEACCKILVDEKEDGGAABEQEETETGOAG 420
Db 361 LEKEGTAGLYRGIGPSCIKLMPAAGISFMCYEACCKILVDEKEDGGAABEQEETETGOAG 420
Qy 421 GOAAPKSSNGDRP 433
Db 421 GOAAPKSSNGDRP 433

RESULT 2

US-10-659-199-18
; Sequence 18, Application US/10659199
; Publication No. US20040038287A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafaleki, Anconl
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/10/659, 199
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/796, 766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 433
; TYPE: PRF
; ORGANISM: Trilicium aestivum
US-10-659-199-18

Query Match 100.0%; Score 2217; DB 15; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.7e-193;

Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAMAATVTVTKNNRASLVMDKKWMLLRPEVAFPMWSQPEBSRLDPFRRALFASVGL 60
Db 1 MAAMAATVTVTKNNRASLVMDKKWMLLRPEVAFPMWSQPEBSRLDPFRRALFASVGL 60
Qy 61 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKORAKKAKKQOLSLRKVRXIGN 120
Db 61 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKORAKKAKKQOLSLRKVRXIGN 120
Qy 121 PHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGADSMAGVPRMTREMGPFGRN 180
Db 121 PHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGADSMAGVPRMTREMGPFGRN 180
Qy 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVP1PTPLVAGALAGVASTLCTYPMEL 240
Db 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVP1PTPLVAGALAGVASTLCTYPMEL 240

Db 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVP1PTPLVAGALAGVASTLCTYPMEL 240
Qy 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Db 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Qy 301 RRASGKEEVGNVPTLLIGSAGAIASATATPPELVARKOMOVAGVGRQVYKNVLHAMYCI 360
Db 301 RRASGKEEVGNVPTLLIGSAGAIASATATPPELVARKOMOVAGVGRQVYKNVLHAMYCI 360
Qy 361 LEKEGTAGLYRGIGPSCIKLMPAAGISFMCYEACCKILVDEKEDGGAABEQEETETGOAG 420
Db 361 LEKEGTAGLYRGIGPSCIKLMPAAGISFMCYEACCKILVDEKEDGGAABEQEETETGOAG 420
Qy 421 GOAAPKSSNGDRP 433
Db 421 GOAAPKSSNGDRP 433

RESULT 3

US-10-425-114-53253
; Sequence 53253, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53253
; LENGTH: 440
; TYPE: PRF
; ORGANISM: Zea mays
; FEATURES:
; OTHER INFORMATION: Clone ID: 700802849_FLI.Pep
US-10-425-114-53253

Query Match 69.0%; Score 1529; DB 15; Length 440;
Best Local Similarity 70.7%; Pred. No. 1.1e-130;

Matches 316; Conservative 37; Mismatches 54; Indels 40; Gaps 9;

Qy 1 MAAMAATVTVTKNNRASLVMDKKWMLLRPEVAFPMWSQPEBSRLDPFRRALFASVGL 58
Db 2 MAAMAATVTVTKNNRASLVMDKKWMLLRPEVAFPMWSQPEBSRLDPFRRALFASVGL 53
Qy 59 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKORAKKAKKQOLSLRKVRXIGN 102
Db 59 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKORAKKAKKQOLSLRKVRXIGN 102
Qy 103 KAKKQO-----LSLRKVRXIGNPHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGAD 158
Db 103 KAKKQO-----LSLRKVRXIGNPHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGAD 158
Qy 159 SMAGVPRMTREMGPFGRN180
Db 159 SMAGVPRMTREMGPFGRN180
Qy 174 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKORAKKAKKQOLSLRKVRXIGN 233
Db 174 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKORAKKAKKQOLSLRKVRXIGN 233
Qy 219 PHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGADSMAGVPRMTREMGPFGRN 278
Db 219 PHLRRLVSGAIIAGVSRFTVAPLETTIRTHLMVSSSGADSMAGVPRMTREMGPFGRN 278
Qy 234 TPLVAGALAGVASTLCTYPMELIKITVITTEKDYDVAHAFVKIYRDEBGPGLYRGLAPSL 293
Db 234 TPLVAGALAGVASTLCTYPMELIKITVITTEKDYDVAHAFVKIYRDEBGPGLYRGLAPSL 293
Qy 279 LIGVVPYAAANFYAETLRGVYKNVLHAMYCI 335
Db 279 LIGVVPYAAANFYAETLRGVYKNVLHAMYCI 335
Qy 294 LIGVVPYAAANFYAETLRGVYKNVLHAMYCI 353
Db 294 LIGVVPYAAANFYAETLRGVYKNVLHAMYCI 353
Qy 336 RKQMOVAGVGRQVYKNVLHAMYCI 395
Db 336 RKQMOVAGVGRQVYKNVLHAMYCI 395

Db 354 KROMOVGAVGRQVQNVHAIYCIILKKGAGGLYRGLSPSCIKLMPAGIAFMCEYACK 413
QY 396 KILVDEKEDGGAAPQETETGOAGGQ 422
Db 414 KILVDEKED-----EEBEDAGGGE 433

RESULT 4
US-10-425-114-50902

/ Sequence 50902, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E.
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 50902
/ LENGTH: 439
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3061-107-H7_F11.pcp
US-10-425-114-50902

Query Match 68.6%; Score 1521.5; DB 15; Length 439;
Best Local Similarity 70.9%; Pred. No. 5,4e-130;
Matches 316; Conservative 38; Mismatches 53; Indels 39; Gaps 10;

QY 1 MAAAAATMTMTKNNRASLVMDKMWLRPEVAPPMSSQ--PESRSLDPPRRALFASVG 59
Db 2 MAATAVTTMTWRS-----KESWSLSQVPAVAFPMKPRGCKTGGLFPRRAMPASVG 53
QY 60 LSLSHGAPP--VAREHDK-ARPAD--DVHQQLAA-----GEAGVQAKQAKK 103
Db 54 LNVCGVAGRPDRPRDPVVAADNCDIARQLGAAPGQAAMEAEBAARRKQGGG 113
QY 104 AKKQO----LSRKRVKIGNPHLRRLVSGAIAGAVSRTFVAPLETIRTHLWVGSGADS 159
Db 114 SKKQOQLDLSLRKRVKIANPRLRLVSGAIAGAVSRTFVAPLETIRTHLWVGSGADS 173
QY 160 MAGVRWIMRTGGMGLPRGNVNVLRVAPSKAIEHFTYDTAKKULTPAGRPAPVPIPT 219
Db 174 MAGVQMTQMGWGLPRGNVNVLRVAPSKAIEHFTYDTAKKULTPAGRPAPVPIPT 233
QY 220 PLVAGALGAVSTLCTYPMEIVKTRLTTEKDYDNLHAFKIVRDEGSGELYRGLAPSL 279
Db 234 PLVAGALGAFSTLCTYPMEIVKTRLTTEKDYDNLHAFKIVRDEGSGELYRGLAPSL 293
QY 280 IGVVYAAANFYAYETLKGVRVRSAGKE--EVGNVPTLLIGSAGAIASATPFLVAR 336
Db 294 IGVVYAAANFYAYETLKGVRVRSAGKE--EVGNVPTLLIGSAGAIASATPFLVAR 353
QY 337 KOMOVGAVGRQVYQNVHAIYCIILKKGAGGLYRGLSPSCIKLMPAGIASMCEYACK 396
Db 354 KOMOVGAVGRQVYQNVHAIYCIILKKGAGGLYRGLSPSCIKLMPAGIASMCEYACK 413
QY 397 ILVDEKEDGGAAPQETETGOAGGQ 422
Db 414 ILVDEKED-----EEBEDAG--GGE 432

RESULT 5
US-10-425-114-65995
/ Sequence 65995, Application US/10425114

/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E.
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 65995
/ LENGTH: 439
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3898-016-B4_F11.pcp
US-10-425-114-65995

Query Match 68.6%; Score 1521.5; DB 15; Length 439;
Best Local Similarity 70.9%; Pred. No. 5,4e-130;
Matches 316; Conservative 38; Mismatches 53; Indels 39; Gaps 10;

QY 1 MAAAAATMTMTKNNRASLVMDKMWLRPEVAPPMSSQ--PESRSLDPPRRALFASVG 59
Db 2 MAATAVTTMTWRS-----KESWSLSQVPAVAFPMKPRGCKTGGLFPRRAMPASVG 53
QY 60 LSLSHGAPP--VAREHDK-ARPAD--DVHQQLAA-----GEAGVQAKQAKK 103
Db 54 LNVCGVAGRPDRPRDPVVAADNCDIARQLGAAPGQAAMEAEBAARRKQGGG 113
QY 104 AKKQO----LSRKRVKIGNPHLRRLVSGAIAGAVSRTFVAPLETIRTHLWVGSGADS 159
Db 114 SKKQOQLDLSLRKRVKIANPRLRLVSGAIAGAVSRTFVAPLETIRTHLWVGSGADS 173
QY 160 MAGVRWIMRTGGMGLPRGNVNVLRVAPSKAIEHFTYDTAKKULTPAGRPAPVPIPT 219
Db 174 MAGVQMTQMGWGLPRGNVNVLRVAPSKAIEHFTYDTAKKULTPAGRPAPVPIPT 233
QY 220 PLVAGALGAVSTLCTYPMEIVKTRLTTEKDYDNLHAFKIVRDEGSGELYRGLAPSL 279
Db 234 PLVAGALGAFSTLCTYPMEIVKTRLTTEKDYDNLHAFKIVRDEGSGELYRGLAPSL 293
QY 280 IGVVYAAANFYAYETLKGVRVRSAGKE--EVGNVPTLLIGSAGAIASATPFLVAR 336
Db 294 IGVVYAAANFYAYETLKGVRVRSAGKE--EVGNVPTLLIGSAGAIASATPFLVAR 353
QY 337 KOMOVGAVGRQVYQNVHAIYCIILKKGAGGLYRGLSPSCIKLMPAGIASMCEYACK 396
Db 354 KOMOVGAVGRQVYQNVHAIYCIILKKGAGGLYRGLSPSCIKLMPAGIASMCEYACK 413
QY 397 ILVDEKEDGGAAPQETETGOAGGQ 422
Db 414 ILVDEKED-----EEBEDAG--GGE 432

RESULT 6
US-10-437-963-150460
/ Sequence 150460, Application US/10437963
/ Publication No. US20040123943A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

Best Local Similarity 65.4%; Pred. No. 4,8e-119;
Matches 291; Conservative 46; Mismatches 69; Indels 39; Gaps 9;

QY 1 MAAAAATTMTTKNNRASLVMDKK-LPPEVPAFPMSSQ--PESLSPERRALPASVG 59
DB 1 MAAATVATMTVRS-----KESWSIQVPVAFPMKPRGKGTGGLFPRRAMPASVG 52
QY 60 LLSHAGAP--VAREHDK-ARPAD--DVAAHQLAAGEAGVQKAKKAKKQOLSLRKV 114
DB 53 LNVCGVPAGRDPREDDPKVRAADNCDLAASLAPFPSPGRPGRCGRSEEEAAGRHH 112
QY 115 RVKIG-----NPHLRRLVSGAIVASRTFVAPLETTIRTHLMVSSGSDSM 160
DB 113 EEAAGRSEPEEGQODRQPARLVSGAIVASRTFVAPLETTIRTHLMVSGSDSM 172
QY 161 AGVPMIMTEGMPGLFRGNANVNLRAVASKAIEHTYDTAKKYLTPKEGPAKVP 220
DB 173 AGVPMIMTEGMPGLFRGNANVNLRAVASKAIEHTYDTAKKYLTPKEGPAKVP 232
QY 221 LVAGALAGVASTLCTYPMELVTKRLTIEKDYDNLHAFAVKIYRDEGPELRYGLAPSLI 280
DB 233 LVAGALAGVASTLCTYPMELVTKRLTIEKDYDNLHAFAVKIYRDEGPELRYGLAPSLI 292
QY 281 GVVPYAAANFYAYETLRGVYRASAQKE--EVGNVPTLLIGSAGAIASATFPLEVARK 337
DB 293 GVVPYAAANFYAYETLRGVYRASAQKE--EVGNVPTLLIGSAGAIASATFPLEVARK 352
QY 338 QMVGAVGGRQYKAVNLHAMCYCLEKEGTAGLYRGISPCIKLMPAAGISFMCYKCKKI 397
DB 353 QMVGAVGGRQYKAVNLHAMCYCLEKEGTAGLYRGISPCIKLMPAAGISFMCYKCKKI 412
QY 398 LVDEKEDGGAEPQETETGQAGGQ 422
DB 413 LVDEKEDGGAEPQETETGQAGGQ 429

RESULT 9
US-10-437-963-146611
; Sequence 146611, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146611
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_47219C.1.pcp
US-10-437-963-146611

Query Match 60.0%; Score 1329.5; DB 16; Length 423;
Best Local Similarity 64.4%; Pred. No. 1.7e-112;
Matches 275; Conservative 47; Mismatches 76; Indels 29; Gaps 8;

QY 1 MAAAAATTMTTKNNRASLVMDKK-LPPEVPAFPMSSQ--PESLSPERRALPASVG 53
DB 1 MAAATVATMTVRS-----KESWSIQVPVAFPMKPRGKGTGGLFPRRAMPASVG 52
QY 54 LPAVGLSLSHGAPVVA--REHDKARPADVVAHQLAA-----GEAGVQK 97

DB 59 LPAVGLSLSHGAPVVA--REHDKARPADVVAHQLAA-----GEAGVQK 118
QY 98 AQKAKKAKKQOLSLRKVRKICGNPHLRRLVSGAIVASRTFVAPLETTIRTHLMVSSGA 157
DB 119 GKAATKAKKRGGL--KTKIKGNPHLRRLVSGAIVASRTFVAPLETTIRTHLMVSSNG- 174
QY 158 DSMAGVFRMIMTEGMPGLFRGNANVNLRAVASKAIEHTYDTAKKYLTPKEGPAKVP 217
DB 175 DSMTEVFQSIKMTGEGTGLFRGNANVNLRAVASKAIEHTYDTAKKYLTPKEGPAKVP 234
QY 218 PPLVAGALAGVASTLCTYPMELVTKRLTIEKDYDNLHAFAVKIYRDEGPELRYGLAP 277
DB 235 PPLVAGALAGVASTLCTYPMELVTKRLTIEKDYDNLHAFAVKIYRDEGPELRYGLAP 294
QY 278 SLIGVVPYAAANFYAYETLRGVYRASAQKEVGNVPTLLIGSAGAIASATFPLEVARK 337
DB 295 SLIGVVPYAAANFYAYETLRGVYRASAQKEVGNVPTLLIGSAGAIASATFPLEVARK 354
QY 338 QMVGAVGGRQYKAVNLHAMCYCLEKEGTAGLYRGISPCIKLMPAAGISFMCYKCKKI 397
DB 355 QMVGAVGGRQYKAVNLHAMCYCLEKEGTAGLYRGISPCIKLMPAAGISFMCYKCKKI 414
QY 398 LVDEKED 404
DB 415 LVDEKED 421

RESULT 10
US-10-425-114-63026
; Sequence 63026, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63026
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73089B03_P1.pcp
US-10-425-114-63026

Query Match 59.1%; Score 1310; DB 15; Length 444;
Best Local Similarity 65.3%; Pred. No. 1.1e-110;
Matches 278; Conservative 48; Mismatches 70; Indels 30; Gaps 11;

QY 1 MAAAAATTMTTKNNRASLVMDKK-LPPEVPAFPMSSQ--PESLSPERRALPASVG 53
DB 25 MAAATVATMTVRS-----KESWSIQVPVAFPMKPRGKGTGGLFPRRAMPASVG 52
QY 54 LPAVGLSLSHGAPVVA--REHDKARPADVVAHQLAA-----GEAGVQK 99
DB 82 LPAVGLSLSHGAPVVA--REHDKARPADVVAHQLAA-----GEAGVQK 140
QY 100 KAKK-AKKQOLSLRKVRKICGNPHLRRLVSGAIVASRTFVAPLETTIRTHLMVSSGAD 158
DB 141 KAKKAKKRGGL--KTKIKGNPHLRRLVSGAIVASRTFVAPLETTIRTHLMVSSNG-D 196
QY 159 DSMAGVFRMIMTEGMPGLFRGNANVNLRAVASKAIEHTYDTAKKYLTPKEGPAKVP 218
DB 197 SMTEVFQSIKMTGEGTGLFRGNANVNLRAVASKAIEHTYDTAKKYLTPKEGPAKVP 256
QY 219 TPLVAGALAGVASTLCTYPMELVTKRLTIEKDYDNLHAFAVKIYRDEGPELRYGLAPS 278

Db 257 PSIIAGALAGVSSITLCYTPPELITRLLIEKDYNNFLHAFVKILREGESELYRGITLPS 316
Qy 279 LIGVVPYAAANFYAYETLRGVYRRASGKEEVGNVPTLLIGSAGAIASATAFPLEVARQ 338
Db 317 LIGVVPYAAANFYAYDTLTKLYRKTFRKQEIISNATLLIGSAGAIASATAFPLEVARQ 376
Qy 339 MOVGAVGROYKYNVLAHMYCILEKEGTAGLYRGIGSPSICIKLMPAAGISFPCYACKKIL 398
Db 377 MOVGAVGROYKYNVLAHMYCILEKEGTAGLYRGIGSPSICIKLMPAAGISFPCYACKKIL 436
Qy 399 VDEKED 404
Db 437 VEDNED 442

RESULT 11

US-10-425-114-63935
; Sequence 63935, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63935
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4738-065-E6_FLI.pep
US-10-425-114-63935

Query Match 59.1%; Score 1310; DB 15; Length 444;

Best Local Similarity 65.3%; Pred. No. 1.1e-110;
Matches 278; Conservative 48; Mismatches 70; Indels 30; Gaps 11;

Qy 1 MAAMAATMTWTNNKNSALVMDKK-NMLLRPVPEVAPFMSQPE---SRSLDF---PRRA 53
Db 25 MAAMVAMTARSKN--SILPMEKQGWSIQ-LPELRFPWDSHEDKFSLSIQSGSPSHG 81
Qy 54 LFASVGLSLSHGAPVA-----REHDKARPADVAHQLAAGEAGVOKA--Q 99
Db 82 LFASVGLKSTGARAVALPGEDKDIKLPFDHCKM-YVSEAVGQVISTEASEVEVDA 140
Qy 100 KAKK-AKKQOISLRKRVKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSGAD 158
Db 141 KAKKAARKRGQL---KIKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSNG-D 196
Qy 159 SMAGVPRMIRTEBMPGLFRGNLVNVRVAPSKAIEHFTYDTAKVLTPEAGEPAKPIR 218
Db 197 SMTEVFOSIMTEBMTGLFRGNLVNVRVAPSKAIEHFTYDTAKVLTPEAGEPAKPIR 256
Qy 219 TPLVAGALAGVASTLCYTPMELVKTRLTIEKDYNDNLHAFVKIVRDEGPGELYRGILAPS 278
Db 257 PSIIAGALAGVSSITLCYTPPELITRLLIEKDYNNFLHAFVKILREGESELYRGITLPS 316
Qy 279 LIGVVPYAAANFYAYETLRGVYRRASGKEEVGNVPTLLIGSAGAIASATAFPLEVARQ 338
Db 317 LIGVVPYAAANFYAYDTLTKLYRKTFRKQEIISNATLLIGSAGAIASATAFPLEVARQ 376
Qy 339 MOVGAVGROYKYNVLAHMYCILEKEGTAGLYRGIGSPSICIKLMPAAGISFPCYACKKIL 398
Db 377 MOVGAVGROYKYNVLAHMYCILEKEGTAGLYRGIGSPSICIKLMPAAGISFPCYACKKIL 436

Qy 399 VDEKED 404
Db 437 VEDNED 442

RESULT 12

US-10-425-114-52078
; Sequence 52078, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52078
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700093540_FLI.pep
US-10-425-114-52078

Query Match 59.0%; Score 1309; DB 15; Length 444;
Best Local Similarity 65.2%; Pred. No. 1.4e-110;
Matches 277; Conservative 47; Mismatches 73; Indels 28; Gaps 10;

Qy 1 MAAMAATMTWTNNKNSALVMDKNMLLRPVPEVAPFMSQPE---SRSLDF---PRRL 54
Db 25 MAAMVAMTARSKNSILP-VEKKQGWSIQ-LPELRFPWDSHEDKFSLSIQSGSPSHGL 82
Qy 55 FASVGLSLSHGAPVA-----REHDKARPADVAHQLAAGEAGVOKA--QK 100
Db 83 FASVGLKSTGARAVALPGEDKDIKLPFDHCKMYP-EAVGQVISTEASEVEVDAK 141
Qy 101 AKK-AKKQOISLRKRVKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSGADS 159
Db 142 AKKAARKRGQL---KIKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSNG-DS 197
Qy 160 MAGVPRMIRTEBMPGLFRGNLVNVRVAPSKAIEHFTYDTAKVLTPEAGEPAKPIR 219
Db 198 MTEVFOSIMTEBMTGLFRGNLVNVRVAPSKAIEHFTYDTAKVLTPEAGEPAKPIR 257
Qy 220 PLVAGALAGVASTLCYTPMELVKTRLTIEKDYNDNLHAFVKIVRDEGPGELYRGILAPSL 279
Db 258 SLIAGALAGVSSITLCYTPPELITRLLIEKDYNNFLHAFVKILREGESELYRGITLPS 317
Qy 280 IGVVVPYAAANFYAYETLRGVYRRASGKEEVGNVPTLLIGSAGAIASATAFPLEVARQ 339
Db 318 IGVVVPYAAANFYAYDTLTKLYRKTFRKQEIISNATLLIGSAGAIASATAFPLEVARQ 377
Qy 340 QVAVGROYKYNVLAHMYCILEKEGTAGLYRGIGSPSICIKLMPAAGISFPCYACKKIL 399
Db 378 QVAVGROYKYNVLAHMYCILEKEGTAGLYRGIGSPSICIKLMPAAGISFPCYACKKIL 437
Qy 400 DEKED 404
Db 438 EDNED 442

RESULT 13

US-10-437-963-122416
; Sequence 122416, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 122416
 LENGTH: 415
 TYPE: PRT
 ORGANISM: *Oryza sativa*
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_25345C.1.pep
 US-10-437-963-122416

Query Match	53.8%	Score 1192;	DB 16;	Length 415;
Best Local Similarity	65.3%	Pred. No. 6e-100;		
Matches 235; Conservative	47;	Mismatches 72;	Indels 6;	Gaps 2

[illegible]

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RESULT 14
US-10-425-114-67044
: Sequence 67044, Application US/10425114
: Publication No. US2004003488A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Jingdong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(5313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 67044
: LENGTH: 431
: TYPE: prt
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: LIB4757-025-G11.F11.pcp

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US-10-425-114-67044

Query Match	51.9%;	Score 1151.5;	DB 15;	Length 431;
Best Local Similarity	63.8%;	Pred. No. 3.2e-96;		
Matches 229;	Conservative 49;	Mismatches 72;	Indels 9;	Gaps 3;

Qy	50	PRALFASVGLSLSHGAPVPAEHHGKARPDD-----VAHQLAAGAAGVQKQAKKAK	105
Db	78	EPAGLFSMGQGVGVGFQPTSSRSPSPETPPDPYMKVYSPPEVETPPSGEGLVLRDGKK	137
Qy	106	KQQLSLRKRVKIGNPHLRLVSGALAGAVSTFPAPLETTIRHLMYSSGADSMAGVFR	165
Db	138	KAV----KIRIKVYVHHKRLISGLAQTVERIVAPLETTIRHLMYGSNG-NSTSEVFQ	192
Qy	166	WIRTEGMPGLFRGNAVNVLRAPSKALEHTYDTAKYLLPEAGSEPAKVIPIPLVAGA	225
Db	193	SLMKHGWMGLFRGNFVAVIRAPSKALELPAFDTANKFLTRKSGBERKIPVPSLVAGA	252
Qy	226	LAGVASTLCTYPMELVKTRLTTEKQVYNLHAAPKYVRDGGPEELRYGLAPSLIGVPR	285
Db	253	PAVASTLCTYPMELVKTRLTIQRVYNFLDAFVKIVRDEGPEELRYGLTPSLIGVPR	312
Qy	286	AAANFAVETTLGVYRRASGKEEVNVTLLISGAAGIASTATPPEVARKQMVGAVG	345
Db	313	AAANFAVDTLKKVYKKQPKTNEIGNVPTLLISGAAGISSAATPEVARKHMVGAVG	372
Qy	346	GROYKNVILHMYCTLEKEGTAGLYRGIGBPCIKLMPAAGISFPCYDAACKKILVDEKD	404
Db	373	GRGVYNNMLHALLSTLEDEGVGGLYKGGSPCKMLMPAAGISFPCYDAACKKILIEEDE	431

RESULT 15
US-09-796-766-20

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? Sequence 20, Application US/09796766
? Patent No. US2001004752A1
? GENERAL INFORMATION:
? APPLICANT: Allen, Steve
? APPLICANT: Rafalski, Antoni
? TITLE OF INVENTION: BRITILE-1 HOMOLOGS
? FILE REFERENCE: BBI157 US CIP
? CURRENT APPLICATION NUMBER: US/09/796,766
? PRIOR FILING DATE: 2001-03-01
? PRIOR APPLICATION NUMBER: 09/668884
? PRIOR FILING DATE: 2000-09-25
? PRIOR APPLICATION NUMBER: PCT/US99/06583
? PRIOR FILING DATE: 1999-03-22
? PRIOR APPLICATION NUMBER: 60/079420
? PRIOR FILING DATE: 1998-03-26
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: Microsoft Office 97
? SEQ ID NO 20
? LENGTH: 289
? TYPE: PRT
? ORGANISM: Trilicium aestivum
? US-09-796-766-20

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	Query Match	51.4%	Score 1139.5;	DB 9;	Length 289;
	Best Local Similarity	74.5%;	Pred. No. 2.2e-95;		
	Matches 216;	Conservative 371;	Mismatches 36;	Indels 1;	Gaps 17.
Qy	115 RYKIGNPHLRIVSGAIGAGVSRFTVPLEITIRTHLVGSSGADSMAGVFPMIRTECMP	174	:::::		
Dd	1 KIKVGNSHLKRLLISGGIAGAVSKRTVAPLEIRHRLHVLGVNSNG-NSTREVPFSINKNEBWT	59			
Qy	175 GLPRGNANVNLRYAAPSKAIIEHFTYDIAKKYLTPRAGEPAKVPIPTPLVAGAIGASTLC	234	:::::		
Dd	60 GLPFGNLMNVIRVAPSKAIELFADTDAKKELTPRKSGEOKIPIPPSILVAGAFAGVSSTLC	119			
Qy	235 TYPMELVKTLTIETEKDYVDNLHAFAVKIVADEGGELLYRGGLAPSLLIGVPPAAANPAYAE	294	:::::		
Dd	120 TYPELKLKTLLTORGYYVDNFLHAFAVKIVAEEGGAELYRGLTPELIGVPPAAANPAYVD	179			

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OM protein - protein search, using sw model

Run on: May 25, 2005, 12:31:55 ; Search time 222 Seconds
(without alignments)
145.599 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217
Sequence: 1 MAAAMAATTMTKNNRASLV.....TETGAGAGAPKSSNGDRP 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2217	100.0	433	4 US-09-796-766-18	Sequence 18, Appl
2	1401.5	63.2	436	4 US-09-796-766-21	Sequence 21, Appl
3	1139.5	51.4	289	4 US-09-796-766-20	Sequence 20, Appl
4	1001	45.2	272	4 US-09-796-766-14	Sequence 14, Appl
5	589.5	26.6	410	4 US-09-796-766-10	Sequence 10, Appl
6	463	20.9	252	4 US-09-796-766-4	Sequence 4, Appl
7	459	20.7	109	4 US-09-796-766-16	Sequence 16, Appl
8	425.5	19.2	469	4 US-09-188-930-339	Sequence 339, App
9	425.5	19.2	180	4 US-09-312-283C-339	Sequence 339, App
10	401.5	18.1	460	4 US-09-796-766-8	Sequence 8, Appl
11	355.5	16.0	320	2 US-08-933-750C-12	Sequence 12, Appl
12	355.5	16.0	320	3 US-09-234-613-12	Sequence 12, Appl
13	355.5	16.0	320	4 US-09-976-594-711	Sequence 711, App
14	355	16.0	269	4 US-09-248-796A-20733	Sequence 20733, A
15	348	15.7	685	4 US-09-949-016-11180	Sequence 11180, A
16	345	15.6	678	4 US-09-949-016-6406	Sequence 6406, Ap
17	341	15.4	447	4 US-09-160-119-4	Sequence 4, Appl
18	332	15.0	674	3 US-09-160-119-2	Sequence 2, Appl
19	318	14.3	207	4 US-09-248-796A-20731	Sequence 20731, A
20	314.5	14.2	227	4 US-09-270-767-32789	Sequence 32789, A
21	314.5	14.2	227	4 US-09-270-767-48006	Sequence 48006, A
22	305.5	13.8	328	3 US-09-068-140A-15	Sequence 10, Appl
23	305.5	13.8	328	3 US-09-068-140A-15	Sequence 10, Appl
24	277.5	12.5	306	4 US-09-248-796A-17738	Sequence 17738, A
25	276.5	12.5	76	4 US-09-796-766-12	Sequence 12, Appl
26	272.5	12.3	302	4 US-09-270-767-33858	Sequence 33858, A
27	272.5	12.3	302	4 US-09-270-767-49075	Sequence 49075, A

28	271.5	12.2	358	4 US-09-270-767-44738	Sequence 44738, A
29	267	12.0	307	4 US-09-248-796A-17597	Sequence 17597, A
30	265	12.0	260	4 US-09-270-767-44590	Sequence 44590, A
31	263	11.9	301	4 US-09-949-016-6865	Sequence 6865, Ap
32	263	11.9	303	4 US-09-949-016-9952	Sequence 9952, Ap
33	260	11.7	298	3 US-08-961-871-10	Sequence 47, Appl
34	258.5	11.7	297	4 US-09-434-354-47	Sequence 47, Appl
35	258.5	11.7	297	4 US-09-709-785-47	Sequence 47, Appl
36	256	11.5	365	4 US-09-270-767-43637	Sequence 43637, A
37	255	11.5	293	4 US-09-248-796A-17601	Sequence 17601, A
38	255	11.5	304	4 US-09-949-016-11339	Sequence 11339, A
39	250	11.3	298	4 US-09-434-354-49	Sequence 49, Appl
40	250	11.3	298	4 US-09-709-785-49	Sequence 49, Appl
41	245.5	11.1	298	4 US-09-248-796A-15499	Sequence 15499, A
42	244.5	11.0	399	4 US-09-248-796A-17636	Sequence 17636, A
43	243	11.0	112	4 US-09-796-766-2	Sequence 2, Appl
44	243	11.0	351	2 US-08-933-750C-19	Sequence 19, Appl
45	243	11.0	351	3 US-09-234-613-19	Sequence 19, Appl

ALIGNMENTS

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RESULT 1
US-09-796-766-18
; Sequence 18, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR APPLICATION NUMBER: 2001-03-01
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-796-766-18

Query Match      100.0%; Score 2217; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.2e-223;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAAAMAATTMTKNNRASLVMDKQMLRPVEVAFPMSSQESRLDPFRRLFPASVGL 60
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61 SLSHGAPVAREHDKARPADVAHQALAAAGAGVOKAKAKAKKQQLSLRKVRKIGN 120
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62 SLSHGAPVAREHDKARPADVAHQALAAAGAGVOKAKAKAKKQQLSLRKVRKIGN 120
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QY 301 RRASGKEEVGNPTLLIGSAAAIATATPELEVARROMOVAGGVYKXVLAHMYCI 360
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DB 301 RRASGKEEVGNPTLLIGSAAAIATATPELEVARROMOVAGGVYKXVLAHMYCI 360
QY 361 LEKGTAGLVKRGDPSCKIIMPAAGISFMCYEAACKIILVDEKEDGAAEPOEETETGOAG 420
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DB 361 LEKGTAGLVKRGDPSCKIIMPAAGISFMCYEAACKIILVDEKEDGAAEPOEETETGOAG 420
QY 421 GOAAPKSSNGDRP 433
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DB 421 GOAAPKSSNGDRP 433
RESULT 2
US-09-796-766-21
; Sequence 21, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Zea mays
US-09-796-766-21
Query Match 63.2%; Score 1401.5; DB 4; Length 436;
Best Local Similarity 65.4%; Pred. No. 6.2e-118;
Matches 291; Conservative 46; Mismatches 69; Indels 39; Gaps 9;
QY 1 MAAAMAATTWTKNNRSLVMDKQWLLRPVEVAFPMWSQ-PRSRSIDPFRALFASVG 59
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DB 1 MAAAMAATTWTKNNRSLVMDKQWLLRPVEVAFPMWSQ-PRSRSIDPFRALFASVG 59
QY 60 LSLSHGAPP--VAEHDGK-ARPAD--DVAHQLAAGBAGVQAKAKKAKKQQLSLRKV 114
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DB 53 LNVCPGVAGRDPRDPKVVRAADNCDIASLAPPPGSRPPGRGRGSEEBEABGRRH 112
QY 115 RVKIG-----NPHLRVSGAIAAGVSTFVAPIETITTHLMVSGGSDSM 160
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DB 113 EEAAGAARSEBEGOGDROPARPARLVSGAIAAGVSTFVAPIETITTHLMVSGIIVDSM 172
QY 161 AGVRWIMRTGMPGLFRGNANVNLRVAPSKAIEHFTYDTAKKYLTPPEAGBPAPVPTP 220
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DB 173 AGVRWIMRTGMPGLFRGNANVNLRVAPSKAIEHFTYDTAKKYLTPPEAGBPAPVPTP 220
QY 221 LVAGALGAVASTLCITYPELVTETLTKEDVYDNLHAFYKIVDESGPGLYRGLASLI 280
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DB 223 LVAGALGAVASTLCITYPELVTETLTKEDVYDNLHAFYKIVDESGPGLYRGLASLI 280
QY 281 GVVVYAAANFYAVETLGGVYRASAQK---EVGNVPTLLIGSAAAIATATPELEVAR 337
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DB 293 GVVVYAAANFYAVETLGGVYRASAQK---EVGNVPTLLIGSAAAIATATPELEVAR 337
QY 338 QMOVGAVGSGROYKXVLAHMYCILEKGTAGLVKRGDPSCKIIMPAAGISFMCYEAACKI 397
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DB 353 QMOVGAVGSGROYKXVLAHMYCILEKGTAGLVKRGDPSCKIIMPAAGISFMCYEAACKI 412
QY 398 LVDEKEDGAAEPOEETETGOAGQ 422
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DB 413 LVDEKED-----EEDEAG--GGE 429
RESULT 3
US-09-796-766-20
; Sequence 20, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-09-796-766-20
Query Match 51.4%; Score 1139.5; DB 4; Length 289;
Best Local Similarity 74.5%; Pred. No. 9.1e-111;
Matches 216; Conservative 37; Mismatches 36; Indels 1; Gaps 1;
QY 115 RVKIGNPHLRVSGAIAAGVSTFVAPIETITTHLMVSGGSDSMAGVRWIMRTGMP 174
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DB 1 KIVGNSHLKRLISGGIAGVSRVVAPIETITTHLMVSGNG--NSTEVFDSIMKQEGWT 59
QY 175 GLFRGNANVNLRVAPSKAIEHFTYDTAKKYLTPPEAGBPAPVPTPVLVAGALGAVASTLC 234
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DB 60 GLFRGNANVNLRVAPSKAIEHFTYDTAKKYLTPPEAGBPAPVPTPVLVAGALGAVASTLC 234
QY 235 TYPELVKTRLTETKEDVYDNLHAFYKIVDESGPGLYRGLASLI GVVVYAAANFYAYE 294
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DB 120 TYPELVKTRLTETKEDVYDNLHAFYKIVDESGPGLYRGLASLI GVVVYAAANFYAYE 294
QY 295 TLEGVYRRASGKEEVGNPTLLIGSAAAIATATPELEVARROMOVAGGVYKXVLAHMYCI 354
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DB 180 TLEGVYRRASGKEEVGNPTLLIGSAAAIATATPELEVARROMOVAGGVYKXVLAHMYCI 354
QY 355 HANYCILEKGTAGLVKRGDPSCKIIMPAAGISFMCYEAACKIILVDEKED 404
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DB 240 HANYCILEKGTAGLVKRGDPSCKIIMPAAGISFMCYEAACKIILVDEKED 404
RESULT 4
US-09-796-766-14
; Sequence 14, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21

SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 272
TYPE: PRT
ORGANISM: Glycine max
US-09-796-766-14

Query Match 45.2%; Score 1001; DB 4; Length 272;
Best Local Similarity 71.3%; Pred. No. 2.7e-96;
Matches 194; Conservative 36; Mismatches 40; Indels 2; Gaps 2;

QY 133 GAVSRTPVAPLETIRTHLMVSSGADSMAGVFRMINTGMPGLFRGNVAVLRVAPSKA 192
DB 3 GAVSRTPVAPLETIRTHLMVSSGADSMAGVFRMINTGMPGLFRGNVAVLRVAPSKA 61
QY 193 IEHFTYDTAKKVTTPRAGEPAKPIPRPLVAGALAGVASTLCTYPPELVKTRLTIEKDY 252
DB 62 IELPAVDYVKQISPPRGEQPIIPIPSSVAGVAGVSSSTLCTYPPELVKTRLTIVRGVY 121
QY 253 DNLHAFAVKIVRDEGGEYRGLAPSLIGVPAANFVAYETLRGVRRASKEEYGNV 312
DB 122 KNLDDFAVRVQEGEPAELYRGLAPSLIGVPAANFVAYETLRKAYKAFKKEEIGNV 181
QY 313 PTLIGSAGALASTATFPLEVARQKQVGVAGVGRQVKNVHAMYCILEKEGTAGLYRG 372
DB 182 MTLIGSAGALISSATFPLEVARQKQVAGALNGRQ-YGNMHALVSIKEEYGVGLYRG 240
QY 373 LGPSCIKLMPADISFMCYACKKILVDEKED 404
DB 241 LGPSCIKLVPADISFMCYACKKRIIVENED 272

RESULT 5

US-09-796-766-10
Sequence 10, Application US/09796766
Patent No. 6660850
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: BBI157 US CIP
CURRENT APPLICATION NUMBER: US/09/796,766
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 410
TYPE: PRT
ORGANISM: Glycine max
US-09-796-766-10

Query Match 26.6%; Score 589.5; DB 4; Length 410;
Best Local Similarity 40.5%; Pred. No. 6.5e-53;
Matches 121; Conservative 74; Mismatches 85; Indels 19; Gaps 5;

QY 118 IENPHLRRLVSGALAGVASTRTFAPLETIRTHLMVSSGADSMAGVFRMINTGMPGLF 177
DB 107 LGSREVRERISGALSAMTKALAPLETIRTRMVV-VGSKINAGSFIVIEEQGQGLM 165
QY 178 RGNVAVLRVAPSKAIEHFTYDTAKKYLTP-----BAGBAPKPIPR-----TPL 221
DB 166 AGNMIMLAIIVTQALELGTFCVCRAKMSLHEKMSNEYPKIQIPIPNINSLSWISV 225
QY 222 -VAGALAGVASTLCTYPPELVKTRLTIEKDYDNLHAFAVKIVRDEGGEYRGLAPSLI 280
DB 226 A1AGAAAGIASTLVCHPFLVDKRLTVSPSETVPSIGIARINLYKQGVGAPYAGISPTLV 285

QY 281 GVVPYAAANFAYETLRGVRRASKEEYGNVPTLLIGSAGALASTATFPLEVARQKQ 340
DB 286 GMLPYSTCFYEMDITKESYCRFKSKSLSRPEMLLIGALAGTASTISPLEVARKRLM 345
QY 341 VGVAGGRQVKNVHAMYCILEKEGTAGLYRGIGPSCIKLMPADISFMCYACKKILV 399
DB 346 VGLAQCK-CPNNVAALSEVIREGLKGLYRGWAGACLAKMPSSGITMWFYEAOKDILL 403

RESULT 6

US-09-796-766-4
Sequence 4, Application US/09796766
Patent No. 6660850
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: BBI157 US CIP
CURRENT APPLICATION NUMBER: US/09/796,766
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 252
TYPE: PRT
ORGANISM: Hordeum vulgare
US-09-796-766-4

Query Match 20.9%; Score 463; DB 4; Length 252;
Best Local Similarity 40.2%; Pred. No. 5.5e-40;
Matches 99; Conservative 55; Mismatches 74; Indels 18; Gaps 4;

QY 175 GFERGNAVAVLRVAPSKAIEHFTYDTAKKYLTP-----BAGBAPKPIPR-----AKVPIPTPL- 221
DB 4 GLWVGNTIMHRIIPQALELGTFCFVVKRGRMSAQEKMEDEGPKQLGNMNIETLHL 63
QY 222 ----VAGALAGVASTLCTYPPELVKTRLTIEKDYDNLHAFAVKIVRDEGGEYRGLAP 277
DB 64 SPVALAGAAAGIAGTLMCHPLEVIXDRLTVDRVTYPSISIAFSKIYRTGIRGLYGLCP 123
QY 278 SLIGVPAANFVAYETLRGVRRASKEEYGNVPTLLIGSAGALASTATFPLEVARK 337
DB 124 TLIGMLPYSTCFYEMDITKESYCRHLHKKSLSRPELLIIGALYGLTASTISPLEVARK 183
QY 338 QMGVAGVGRQVKNVHAMYCILEKEGTAGLYRGIGPSCIKLMPADISFMCYACKKILV 397
DB 184 RLWVGLAQCK-CPNNVAALSEVIREGLGLYIRGWSACLAKMPSSGITMWFYEAOKDI 242
QY 398 LVDEKE 403
DB 243 LLAERD 248

RESULT 7

US-09-796-766-16
Sequence 16, Application US/09796766
Patent No. 6660850
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: BBI157 US CIP
CURRENT APPLICATION NUMBER: US/09/796,766
CURRENT FILING DATE: 2001-03-01

```
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (104)
US-09-796-766-16
```

```
Query Match 20.7%; Score 459; DB 4; Length 109;
Best Local Similarity 84.0%; Pred. No. 4e-40;
Matches 89; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 1 MAAAMATTWTKNNRASLVMDKQWLLRPVEVAFPMSSQPESSSLDFPRRALFASVGL 60
D 1 MAAAMATTWTKNNRASLVMDKQWLLRPVEVAFPMSSQPESSSLDFPRRALFASVGL 60
QY 61 SLSHGAPPVAREHDKARPADVAHQLAAGAGVOKAKAKKAKK 106
D 61 SLSHGAPPVAREHDKARPADVAHQARIRGRGPRGPEBECKKQX 106
```

RESULT 8

```
US-09-188-930-339
; Sequence 339, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Mathew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188.930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-339
```

```
Query Match 19.2%; Score 425.5; DB 3; Length 469;
Best Local Similarity 29.0%; Pred. No. 1.2e-35;
Matches 117; Conservative 63; Mismatches 149; Indels 75; Gaps 10;
```

```
QY 6 AATTMTKNNRASLVMDKQW---LLRPV---PEVAFPMSSQPESSSLDFPRRALFASV 58
D 119 AEKILKMDKNGTMTIDMNEWRDYLHLHPVENIPEITLLYV----- 158
QY 59 GLSLSHGAPPVAREHDKARPADVAHQLAAGAGVOKAKAKKQOLSIRKRVKI 118
D 159 -----KSTIFDVGENLTVPDEFTYBERQTGM----- 185
QY 119 GNPHLRLVSGAIGAVSRFTVAPLETTIRTHLMVSSGADSM--AGVFRWIMRTEGMPGL 176
D 186 ---WMRHLVAGGAGAVSRCTAPDLRLKVLMOVHASRSNNMCI VGGFTQMIREGAKSL 242
QY 177 FRGNAVTVLRVAPSKAIEHFTYDTAKKYLTPKAGEPAKVPIPTLVAGALAGVASTLCY 236
D 243 WRGGINVLKTIAPSAIKFMAVEQMKRLV---GSDQETLRIHRLVAGSLAGALAGSSIT 299
```

```
QY 237 PHELVTKRLTIER-DVYDNLHAFFVKIVRDEGGELRYGLAPSLIGVPPYAAAFYAYET 295
D 300 PHEVLKTRMALRTGTGYSGLDCARRILAKESGAAFYKGIPTMLGIIPYAGIDLAVYET 359
QY 296 LRGVY--RRASGKEEVGNVPTLLIGSAAAGIASTATPELVARKOMQVGA--VGRQVYK 351
D 360 LKNTWLOQRYAVNSADGVFLLACGTISSTCGGLASYPALVTRRQQAQASISGAPVYTM 419
QY 352 NVLHAWYCILEKEGTAGLYRGLGPSCKLMPAAGISFMCYBACK 395
D 420 SSLFKQ--ILRTEGAGLYRGLAPNFMKVI PAVISIVYVENLK 461
```

RESULT 9

```
US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Mathew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312.283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-339
```

```
Query Match 19.2%; Score 425.5; DB 4; Length 469;
Best Local Similarity 29.0%; Pred. No. 1.2e-35;
Matches 117; Conservative 63; Mismatches 149; Indels 75; Gaps 10;
```

```
QY 6 AATTMTKNNRASLVMDKQW---LLRPV---PEVAFPMSSQPESSSLDFPRRALFASV 58
D 119 AEKILKMDKNGTMTIDMNEWRDYLHLHPVENIPEITLLYV----- 158
QY 59 GLSLSHGAPPVAREHDKARPADVAHQLAAGAGVOKAKAKKQOLSIRKRVKI 118
D 159 -----KSTIFDVGENLTVPDEFTYBERQTGM----- 185
QY 119 GNPHLRLVSGAIGAVSRFTVAPLETTIRTHLMVSSGADSM--AGVFRWIMRTEGMPGL 176
D 186 ---WMRHLVAGGAGAVSRCTAPDLRLKVLMOVHASRSNNMCI VGGFTQMIREGAKSL 242
QY 177 FRGNAVTVLRVAPSKAIEHFTYDTAKKYLTPKAGEPAKVPIPTLVAGALAGVASTLCY 236
D 243 WRGGINVLKTIAPSAIKFMAVEQMKRLV---GSDQETLRIHRLVAGSLAGALAGSSIT 299
QY 237 PHELVTKRLTIER-DVYDNLHAFFVKIVRDEGGELRYGLAPSLIGVPPYAAAFYAYET 295
D 300 PHEVLKTRMALRTGTGYSGLDCARRILAKESGAAFYKGIPTMLGIIPYAGIDLAVYET 359
QY 296 LRGVY--RRASGKEEVGNVPTLLIGSAAAGIASTATPELVARKOMQVGA--VGRQVYK 351
D 360 LKNTWLOQRYAVNSADGVFLLACGTISSTCGGLASYPALVTRRQQAQASISGAPVYTM 419
QY 352 NVLHAWYCILEKEGTAGLYRGLGPSCKLMPAAGISFMCYBACK 395
D 420 SSLFKQ--ILRTEGAGLYRGLAPNFMKVI PAVISIVYVENLK 461
```

```
RESULT 10
US-09-796-766-8
; Sequence 8, Application US/09796766
```

```
/ Patent No. 6660850
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Lightner, Jonathan
/ APPLICANT: Ratajski, Antoni
/ TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
/ FILE REFERENCE: BB1157 US CIP
/ CURRENT APPLICATION NUMBER: US/09/796,766
/ CURRENT FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/668884
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: PCT/US99/06583
/ PRIOR FILING DATE: 1999-03-22
/ PRIOR APPLICATION NUMBER: 60/079420
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 8
/ LENGTH: 180
/ TYPE: PRT
/ ORGANISM: Glycine max
/ US-09-796-766-8

Query Match      18.1%; Score 401.5; DB 4; Length 180;
Best Local Similarity 44.4%; Pred. No. 9.1e-34;
Matches 79; Conservative 42; Mismatches 56; Indels 1; Gaps 1;

QY 222 VAGALAGVASTCTYPMELVKTRLTIEKQVYDNLHAFVKIYRDESGPGLYRGLASLIG 281
DB 1 IGAAGAAGIATVCHLEVLKDLRTIVSPETYSIGIAIRNIYDGGVGFYAGISPTLVG 60

QY 282 VVPAANFAYETLRGVRRASGKEVGNVPTLLIGSAAAGIATATPPLVARRKQMV 341
DB 61 MIPYSTCFYFWDITKESYCRKSKSLRPEMLIGALGFTASTISPLEVARRRLMV 120

QY 342 GAVGROVKYKNVLMAMYCIIEKEGTAGLYRGLGSPSCIKLMPAAGISFMCYEACKILV 399
DB 121 GALQOK-CPNNMAALSEVIREBGLKGLRGWCAASCLXMPSSGITMWTYEMKQDLL 177

RESULT 11
US-08-933-750C-12
/ Sequence 12, Application US/08933750C
/ Patent No. 5932442
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Shah, Purvi
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Yue, Henry
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
/ NUMBER OF SEQUENCES: 98
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,750C
/ FILING DATE: September 23, 1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
```

```
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TEXT:
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: SPLNOT02
/ CLONE: 207452
/ US-08-933-750C-12

Query Match      16.0%; Score 355.5; DB 2; Length 320;
Best Local Similarity 30.3%; Pred. No. 1.5e-28;
Matches 89; Conservative 62; Mismatches 120; Indels 23; Gaps 8;

QY 120 NPHLRVLSGALAGAVSRFTVAPLETIRTHLVGS---SGADSWA---GVF---RWIMRT 170
DB 13 NTKFOVAVAGSVSGVLTTRLLISPFVYIKRFOLOHERLSRSPSAKYHGLQASRQILOE 72

QY 171 ECPMGLFRGNANVNLRVAPSKAIEHFTYDTAKKYLTPPEAGBPAKVPIPTLVAGALAGVA 230
DB 73 BGPTAFWKGHVPAQGLISLIGYAVQFLSFEMLELVARGSVYDAR-BFSVHPFCGGLAACM 131

QY 231 STLCTYPMELVKTRLTIEKQVYDNLHAFVKIYRDESGPGLYRGLASLIGVDPYAA 288
DB 132 ATLTVHPVDVLTTRPAQCEPRVYNTLRHAVGTMVRSBGPVFKGLAETLLAIFPYAGL 191

QY 289 NFVAYETLRGVYR---RASGKEVGNVPTLLIGSAAAGIATATPPLVARRKQMV--- 342
DB 192 QPSCYSLHLYKMAIPBEGKKN-EYLOVLLGSGGAGVISKTLTTPLDL-FKRLOVGGFE 250

QY 343 ---AVGROVKYKNVLMAMYCIIEKEGTAGLYRGLGSPSCIKLMPAAGISFMCYE 392
DB 251 HABAAPFGQVRRYKGLMDCAKQVLTQKEGALGFPKGLSPSLKXALSTGFMFPGYE 304

RESULT 12
US-09-234-613-12
/ Sequence 12, Application US/09234613
/ Patent No. 6132973
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Shah, Purvi
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Yue, Henry
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
/ NUMBER OF SEQUENCES: 98
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
```



```
RESULT 15
US-09-949-016-11180
; Sequence 11180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11180
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11180

Query Match      15.7%; Score 348; DB 4; Length 685;
Beet Local Similarity 27.5%; Pred. No. 2.9e-27;
Matches 106; Conservative 73; Mismatches 163; Indels 44; Gaps 12;

QY      75 GKARPAD-DVAHQLA-----AGE---AGVOK-AQKAKKAKKQOLS--LRKVRKIGNP-- 121
DB      268 GGVTLLEIDILYQLADLVNAGSLTLADIERIAPLAEGALPYNIAELQROSPGLGRPIW 327
QY      122 -----HLRLVSGAIAAGAVSRTFVAPLETIRTHLVGSSGADSMAG-----VERWI 167
DB      328 LQIASAVRFTLGSAVAGAVATAYVPIDIVKTR-MQNGRSGSVGELMYKNSPDCFKY 386
QY      168 MREGMPLGFRGNANVLRVAPSKAIEHTYDTAKKYLTPPAGEPAKVPITPPLVAGALA 227
DB      387 LRYEGPFGYRGLIPQLIGVAPEKAIKLVNDPVRDKFTTRDG---SVPLPAEVLGGCA 443
QY      228 GVASTLCTYPMELVTRLTIEKDVYDNILHAFVKIVRDEGPGLYRGLAPSLIGVPPYA 287
DB      444 GGSQYIFPTNPLEIVIRLQVAGEITTPRVSAINVLRDGLTFGLYKGAACFLRDIPSA 503
QY      288 ANFYAYETLRGVYRRASGKEVGNVPTLLIGSAGAIASATATPPLVARKQOVAGVGR 347
DB      504 IYFPYAHCKLIADENG--HYGGLNLAAAGAVPASPVLTPADVIRKIRLQVABAGO 561
QY      348 QYKRVNLHAMYCILEKEGTAGLYRGLGPECITLMPAGISPMCYENCKKILVDEKEDGA 407
DB      562 TTYSGVLDICFRKILREEGSPAFWKGTAAVFRSSPOFGVTLVYELLQRFY---IDFGG 618
QY      408 AEPQETETGAGGQAAPKSSNGDRP 433
DB      619 LKP-----AGSEPTPKSRIADLP 636
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Search completed: May 25, 2005, 14:28:39
Job time : 223 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 25, 2005, 12:24:45 ; Search time 259 Seconds
(without alignments)
160.857 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217

Sequence: 1 MAAAMAATMTYKNNRASLV.....TETGOAGGQAPPKSSNGDRP 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1401.5	63.2	436	JQ1459	Bt1 protein precursor
2	1041	47.0	392	T05350	adenylate transloc
3	462.5	20.9	352	T01729	mitochondrial soln
4	454	20.5	475	T50686	peroxisomal Ca-dep
5	437	19.7	326	S57544	probable membrane
6	421	19.0	479	T49871	peroxisomal Ca-dep
7	418	18.9	332	T47703	Ca-dependent solut
8	418	18.9	358	T45934	hypothetical prote
9	410	18.5	448	D84798	probable mitochond
10	409.5	18.5	318	B96811	hypothetical prote
11	409	18.4	294	T22145	hypothetical prote
12	403	18.2	325	T04273	hypothetical prote
13	403	18.2	415	T48171	hypothetical prote
14	394.5	17.8	330	S26596	Graves disease mit
15	391	17.6	588	T22688	hypothetical prote
16	380	17.1	381	T51158	hypothetical prote
17	361	16.3	326	B40141	mitochondrial soln
18	348	15.7	349	A40141	mitochondrial soln
19	337.5	15.2	531	G89677	protein F17B5.2 (1
20	337.5	15.2	587	T21074	hypothetical prote
21	324	14.6	500	T39385	probable mitochond
22	319.5	14.4	331	T00582	probable mitochond
23	318	14.3	357	S46795	hypothetical prote
24	315	14.2	335	S50453	hypothetical prote
25	308.5	13.9	781	A86205	hypothetical prote
26	305.5	13.8	902	S54495	probable carrier p
27	302	13.6	326	T37874	probable mitochond
28	286.5	12.9	300	T15206	hypothetical prote
29	285.5	12.9	309	T29225	hypothetical prote

30	282.5	12.7	313	2	T23207	hypothetical prote
31	282.5	12.7	373	2	S48451	probable membrane
32	280.5	12.7	313	2	T25850	hypothetical prote
33	280	12.6	377	2	S35081	probable carrier p
34	280	12.6	447	2	T00435	probable mitochond
35	278.5	12.6	291	2	T37992	ADP,ATP carrier pr
36	277.5	12.5	305	2	S68154	ADP,ATP carrier pr
37	277.5	12.5	702	2	T16533	hypothetical prote
38	277	12.5	314	2	S64401	probable membrane
39	275	12.4	309	2	A24849	ADP,ATP carrier pr
40	274.5	12.4	311	2	G86383	probable mitochond
41	270.5	12.2	318	1	A31978	ADP,ATP carrier pr
42	270	12.2	313	1	XNMC	ADP,ATP carrier pr
43	270	12.2	339	2	A41677	ADP,ATP carrier pr
44	269	12.1	322	2	T40526	adp/atp translocas
45	269	12.1	386	2	T09709	ADP,ATP carrier pr

ALIGNMENTS

RESULT 1
JQ1459
Bt1 protein precursor - maize
C/Species: Zea mays (maize)
C/Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C/Accession: JQ1459
R/Sullivan, T.D.; Strelow, L.I.; Illingworth, C.A.; Phillips, R.L.; Nelson Jr., O.E.
Plant Cell 3, 1337-1348, 1991
A/Title: Analysis of maize little-1 alleles and a defective suppressor-mutator-induced
A/Reference number: JQ1459; MUID:93005685; PMID:166652
A/Accession: JQ1459
A/Molecule type: mRNA
A/Residues: 1-436 <SU>
A/Cross-references: UNIPROT:P29518; GB:M79333; NID:g168425; PIDN:AAA33438.1; PID:g168426
C/Comment: This protein acts as an adenylate translocator in amyloplasts.
C/Genetics:
A/Introns: 206/3; 260/3
C/Superfamily: Bt1 protein; ADP,ATP carrier protein repeat homology
C/Keywords: Chloroplast; duplication; transmembrane protein
F/1-75/Domain: transit peptide (amyloplast) #status predicted <TNP>
F/76-436/Product: Bt1 protein #status predicted <MAT>
F/131-217/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F/226-312/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F/323-413/Domain: transmembrane #status predicted <TM1>
F/327-347/Domain: transmembrane #status predicted <TM2>
Query Match 63.2% Score 1401.5; DB 2; Length 436;
Best Local Similarity 65.4% Pred. No. 8.3e-99;
Matches 291; Conservative 46; Mismatches 69; Indels 39; Gaps 9;
QY 1 MAAAMAATMTYKNNRASLVMDKKMLRPDEVAFPPSSQ--PEERSLDFPRALFASVG 59
DB 1 MAAATMAATMTWTRS-----KESWSSLQVPAPVAFPPKPRGGKTCGLFPPRAMPASVG 52
QY 60 LSLSHGAPP--VAREHDK-ARPAD--DVAHQLAAGAGVQAKAKKAKKQQLSLRV 114
DB 53 LNVCGVAGRDPRDPKVVRAADNCDIAASLAPPPGSRPRGRGSGSEBEAEGRNH 112
QY 115 RYKIG-----NHLRLVSGAIALAGAVSRFPVAPLEFIRTHLMVGGSGADSM 160
DB 113 BEAAAAGSEBEEGGODROPAPAPALVSGAIALAGAVSRFPVAPLEFIRTHLMVGSIGVSM 172
QY 161 AGVPRWIRTRGMPGLFRGNVNVLRVAPSKAIEFTYDTAKKYLTPEAGSPAKVPIPTP 220
DB 173 AGVPRWIRTRGMPGLFRGNVNVLRVAPSKAIEFTYDTAKKYLTPEAGSPAKVPIPTP 232
QY 221 LVAGLAGVASTLCTYPMELVKTRLTTEKDYVDMLLHAFAVIVRDEGSELYRGLAPSLI 280
DB 223 LVAGLAGVASTLCTYPMELVKTRLTTEKDYVDMLLHAFAVIVRDEGSELYRGLAPSLI 292
QY 281 GVPRYAAANFYAETLRGVYRRASGE--EVGNVPTLLIGSAAGALSTATPFLVAVRK 337

```
Db      293 GVPYACNFAVETTLRLYRATGRPRGADVGVATLLIGSAGAIASATPELEVARK 352
      338 QMOVGANGROVKNVYHAMVCTLEKEGTAGLVRGAGPSCTKMPAAGISPMCEACCKI 397
      353 QMOVGANGROVKNVYHAMVCTLEKEGTAGLVRGAGPSCTKMPAAGISPMCEACCKI 412
      398 LVDEKEDGAAEPOEETETGQAGQ 422
      413 LVDEKEDS-----EEDDEAG--GGE 429

RESULT 2
T05350
adenvylate translocator britle-1 homolog F8B4.100 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T05350
R/Bevan, M.; Terry, N.; Ardiiles, W.; Buysbaert, C.; Daseeville, R.; De Clerck, R.; De
ewes, H.M.; Mayer, K.F.X.; Schueller, C.
Submitted to the Protein Sequence Database, February 1999
A/Reference number: Z15409
A/Accession: T05350
A/Molecule type: DNA
A/Residues: 1-392 <BEV>
A/Cross-references: UNIPROT:Q9SUU1; EMBL:AL034567
A/Experimental source: cultivar Columbia; BAC clone F8B4
C/Genetic:
A/Map position: 4
A/Intons: 181/3; 235/3
A/Note: F8B4.100
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Query Match 47.0%; Score 1041; DB 2; Length 392;
Best Local Similarity 64.9%; Pred. No. 1.8e-71;
Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

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QY      92 EAGVQAKQAKKAKKQOLSLRKVRVKIGNPHLRRLVSGAINGAVSRTPVAPLETIRTHM 151
      83 EEEVNVNKKRKKKKGGTLT--KIKTANPSLRRLLSGAVAGVSRTPVAPLETIRTHM 139
      152 VGSAGDSMAGVFWIRKTEGMPGLFRGNANVNLRVAPSKAIEHTYDTAKYITPEAGE 211
      140 VG-SGNSSTVEFDIMKHEGWTGLFRGNLVNVRVAPARAVELFVEETVAKKLSPPHQ 198
      212 PAKPIPTPLVAGALVASTLCYPMELVTRLTITKDYDNLNLAHFKVIRDEGPEL 271
      199 ESKPIPTPLVAGALVASTLCYPMELVTRLTITKDYDNLNLAHFKVIRDEGPEL 258
      272 YRGAPSLIGVPPAANFYAETLRGVRRASKEEYGVNPTLLIGSAGAIASATPFP 331
      259 YRGAPSLIGVPPAANFYAETLRGVRRASKEEYGVNPTLLIGSAGAIASATPFP 318
      332 LEVARKQMOVGANGROVKNVYHAMVCTLEKEGTAGLVRGAGPSCTKMPAAGISPMCY 391
      319 LEVARKQMOVGANGROVKNVYHAMVCTLEKEGTAGLVRGAGPSCTKMPAAGISPMCY 378
      392 EACKKILVDEKED 404
      379 EACKKILINNQS 391

Db
```

RESULT 3
T01729
mitochondrial solute carrier protein homolog - Arabidopsis thaliana
N/Alternate names: protein A_IG002N01.16
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C/Accession: T01729
R/Scheet, P.; Maggi, L.
Submitted to the EMBL Data Library, June 1997
A/Description: The sequence of A. thaliana IG002N01.
A/Reference number: Z14407
A/Accession: T01729

A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-352 <SCH>
A/Cross-references: UNIPROT:Q04619; EMBL:AF007269; NID:g2191126; PID:g2191150
A/Experimental source: cultivar Columbia
C/Genetic:
A/Map position: 4
A/Intons: 51/2; 67/3; 122/2; 135/1; 172/3; 210/3; 325/3
A/Note: A_IG002N01.16
C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C/Keywords: mitochondrion

Query Match 20.9%; Score 462.5; DB 2; Length 352;
Best Local Similarity 33.8%; Pred. No. 1.4e-27;
Matches 120; Conservative 62; Mismatches 124; Indels 49; Gaps 12;

```
QY      80 ADDVANAQLAAGAGVQKQAKK-AKQOLSLRKVRVKIGNPHLRRLVSGAINGAVSRTP 138
      3 SEDVKTESAASVTYNLBEAREGVADPSYAKSI-----CKSLPAGVAGVSRK 54
      139 FVAPLETIRTHLMVGSAGDSMAGV--FWIRKTEGMPGLFRGNANVNLRVAPSKAIEH 195
      55 AVAPLERMKTLLOVQPNHNIKSGVQGLKHIRTETGLGLFGNGCTNCARIVNSAVKF 114
      196 FTYDTAKK----YLTPEAGEPAKVPDIPPLV--AGALVASTLCYPMELVTRLT 247
      115 FSYEQASNGILVYRORTGENAQL---TPLRLAGATAGTAMGATVPMWRGRRLTV 171
      248 EKD----VVDNLHAHVVKVLRDESGPELVRLGLAPSLIGVPPAANFYAETLRG--VVR 301
      172 QTNAPYQYRGIMHAAVLRREGRPALTRGMPLSYIVGVPPVGLNFSYTESKDLVKE 231
      302 RASG--KKEEVGNVPTLLIGSAGAIASATPPELEVARKOMOVGAVG-----GR 347
      232 NPYGLVNNELTYVTLLTGALVGTQGTAYPLDVIRRMQW--VGMKDSALVTGEGR 289
      348 QV---YKONVLAHVCTLEKEGTAGLVRGAGPSCTKMPAAGISPMCEACCKIL 398
      290 STASLEYTGWVDAFRKTVRHEGFGALVKGIVPNSKVVPISALAFVYEMVKDVL 344

Db
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RESULT 4
T50686
peroxisomal Ca-dependent solute carrier [imported] - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C/Accession: T50686
R/Weber, F.B.; Minestrini, G.; Dyer, J.H.; Weider, M.; Boffelli, D.; Compassi, S.; Wehr
Proc. Natl. Acad. Sci. U.S.A. 94, 8509-8514, 1997
A/Title: Molecular cloning of a peroxisomal Ca2+-dependent member of the mitochondrial
A/Reference number: Z25180; NUID:97385133; PMID:9238007
A/Accession: T50686
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-475 <WEB>
A/Cross-references: UNIPROT:O18757; EMBL:AF004161; PIDN:AA69156.1
C/Keywords: peroxisome

Query Match 20.5%; Score 454; DB 2; Length 475;
Best Local Similarity 36.5%; Pred. No. 9.1e-27;
Matches 103; Conservative 63; Mismatches 102; Indels 14; Gaps 6;

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QY      124 RRLVSGAINGAVSRTPVAPLETIRTHLMVGSAGDSMAGVFWIRKTEGMPGLFRGNANV 183
      196 ROLLAGIAGAVSRTPVAPLETIRTHLMVGSAGDSMAGVFWIRKTEGMPGLFRGNANV 255
      184 VLRVAPSKAIEHTYDTAKKYLTPPEAGEPAKVPDIPPLVAGALVASTLCYPMELVKT 243
      256 VIKIAPETAVKFMVVEQYKLLTEEG--QKIGFERFISGMAAGATAGTFIYPMEMVKT 312
      244 RLITRK-DVYDNLNLAHFKVIRDESGPELVRLGLAPSLIGVPPAANFYAETLRGVYRR 302
      313 RLAVGKTGYSGIYDCAKKILKYGFGAFYKGVPPNLLGIIPYAGIDLAVAYELKSHMD 372

Db
```


A:Residues: 1-418 <STO>
 A:Cross-references: UNIPROT:Q9C9R4; GB:AE005173; NID:96587866; PIDN:AAF18552.1; GSPDB:GN
 C:Species: *Caenorhabditis elegans*
 A:Gene: T1111.12
 A:Map position: 1

Query Match 18.5%; Score 409.5; DB 2; Length 418;
 Best Local Similarity 29.1%; Pred. No. 1.9e-23;
 Matches 121; Conservative 69; Mismatches 159; Indels 67; Gaps 12;

39 SQPESRSGLDFPRRLPASVGLSLSHGAPVAREH-----DGKA 77
 12 SSSSTSTSIDLNEAFSTGGLFLE--PPGVSSSPFDSISSKCSDBEPLHFGYWRNKT 68
 78 RRAADVQHQLAAGEGVGKAKKAKKQQLSL-----KRVKIGNPRLR-----RL 126
 69 RLRSGNMFELSVLSKDRSEQQCKALANDEIPKDNKRKSVIGGVRRRGTMTRKIL 128
 127 VSGALAGAVSRTPVAPLETIRTHLMVSSGADSMAGVFRMIRTEGMPGLFRGNANVLR 186
 129 MAGAVAAVMSKTFIAPLERLKLLEYTRGQRNLV-VAASIAITQGLTFPMKGNLNLVLR 187
 187 VAPSKAIEHFTYDTAKKYLTPBAGEPAKVPITPLVAGALAGVASTLCTYPMELVTRLT 246
 188 TAPFKAIVFCAYDIYRKQLKLAGNQEATNFER-FVAGAAAGITATVLCPLDITRTKL 246
 247 IE-KQVYDNLHAFVKIYVDESGELYRGLAPSLIGVYVYAAANFAVYETLAGVY----- 300
 247 ARGELAGIGAFRYMIQTGLFSLYKGLVPSISMSALSGAVFYGVVDILKSSFLATPE 306
 301 -----RRASGE-----EVGNVPTLLISAGALASTATPPLVARKOMOVGAVG 346
 307 GKRLLDMKQGOELNALDRLEIGPRTIMYGAIACTEVATTPPEVVRQIQM----- 361
 347 RQVYKQVNLHAM--CYLIEKEGTAGLYRGLGSPCICLMPAGISFMCYACKKILV 399
 362 -QMGKNTNALAMGFNIIRGGIPALYAGLLPSLLQVLSASISYVVE-CMKIVL 415

RESULT 11

T22145
 hypothetical protein F43G9.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22145
 R:Kerhavi, J.
 submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19523
 A:Accession: T22145
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-294 <ML>
 A:Cross-references: UNIPROT:Q93717; EMBL:Z79755; PIDN:CAB02107.1; GSPDB:GN00019; CESP:F4
 A:Experimental source: clone F43G9
 C:Species: *Caenorhabditis elegans*
 A:Map position: 1
 A:Introns: 7/3; 44/1; 106/2; 175/1; 201/3; 254/1
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 18.4%; Score 409; DB 2; Length 294;
 Best Local Similarity 34.3%; Pred. No. 1.3e-23;
 Matches 96; Conservative 65; Mismatches 101; Indels 10; Gaps 10;

126 LVSGAIGAVSRTPVAPLETIRTHLMVSSGADSMAGVFRMIRTEGMPGLFRGNANVLR 182
 18 LSAGAIAGALAKTTIAPLDRTKIYQVSSSTRGVSPSAIKFKITLYRRENGFALYKNSA 77
 183 NVLRVAPSKAIEHFTYDTAKKYLTPBAGEPAKVPITPLVAGALAGVASTLCTYPMELV 241
 78 TMAVIVPVYMSQFPAFEGYKLLKLVDENG--SRTPVKR-YINGSLAATATATITVPLDTR 134
 242 KTRLTIEKQV-YDNLHAFVKIYVDESGPELVRGLAPSLIGVYVYAAANFAVYETLRGVY 300

135 KARLSVSSKLYQSSIKHVFVKTYKEGQIQLYRGIVPTLIGVYPYAGSSFFTYETLKIMY 194
 301 RASGKEVGNVPTLLISAGALASTATPPLVARKOMOVAV-CGRVYKQVNLHAMVC 359
 195 RDHREBE-NSYYRNLFGMLAGLIGQSSSPYLDIVRRMQTRISGMSPLRLIH---- 249
 360 ILEKEG-TAGLYRGAGSPCICLMPAGISFMCYACKKIL 398
 250 IYHTEGLKRGLYKLSMMLKGPVAVGVSTTYE--KVL 286

RESULT 12

T04273
 hypothetical protein F20B18.290 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T04273
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohleisel, J.; Mewes, H.W.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15263
 A:Accession: T04273
 A:Molecule type: DNA
 A:Residues: 1-325 <BEV>
 A:Cross-references: UNIPROT:Q9SZ19; EMBL:AL049483
 A:Experimental source: cultivar Columbia; BAC clone F20B18
 C:Genetics:
 A:Map position: 4
 A:Introns: 46/3; 144/3; 181/1; 242/3; 284/3
 A>Note: F20B18.290
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 18.2%; Score 403; DB 2; Length 325;
 Best Local Similarity 31.1%; Pred. No. 4.2e-23;
 Matches 97; Conservative 66; Mismatches 117; Indels 32; Gaps 9;

124 RLTVSAGIAGAVSRTPVAPLETIRTHLMVSSGAD-----SMAGVFRMIRTEGMPGLR 178
 19 KELINGGYTGIGAKTAVAPLERIK--ILFQRRBEPKRIAGVGSINKTKTEGLMGFPR 75
 179 GNAVNLVAPSKAIEHFTYDTAKKYLTPBAGEPAKVPITPLVAGALAGVASTLCTYPM 238
 76 GNGASVARIIVFPAALHMAVMEYRRMIFGPDTRGRL-LDLVAGSFAGTAVLFTYPL 134
 239 ELVKTTRLT-----IEKVDYDNLHAFVKIYVDESGELYRGLAPSLIGVYVYAAAN 289
 135 DLVRYTKLAVYQTCVKAIPEVQIYRGIVCFSTRYSBSGARGLYRGVAPSLYGIFFYAGLK 194
 290 FYAVETLGVARRASGKEVGNVPTLLISAGALASTATPPLVARKOMOV-----GAVG 345
 195 FYFYEEMK--RHVPENKODISLKLVCSSVAGLQTLTTPLDVVRKMOVRLYSANV- 250
 346 GRQVYKQVNLHAMVCYILEKEGTAGLYRGLGSPCICLMPAGISFMCYACKKILVDEKED 404
 251 KEETRGIMQTLFKIARBSGKQLFSGLSINLVKVVPSVAILFTYDIDKHLARVPRR- 309
 405 GGAEPQESTET 416
 310 ----SPEBAVAV 317

RESULT 13

T48171
 hypothetical protein F7A7.20 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T48171
 R:Bevan, M.; Tetlow, N.; Ardiles, W.; Buysheart, C.; Daseville, R.; De Clerck, R.; De
 ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24487
 A:Accession: T48171
 A:Status: preliminary

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 06:55:40 / Search time 1054 Seconds
(without alignments)
158.887 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217
Sequence: 1 MAAAMAATTMTYKNNRASIV.....TETGAGGQAPAKSSNGDRP 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_16Dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20038:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1139.5	51.4	289	2	AAV31936 Wheat brl
2	1041	47.0	316	3	AAQ49412 Arabidops
3	1041	47.0	316	3	AAQ11516 Arabidops
4	1041	47.0	392	3	AAQ11515 Arabidops
5	1041	47.0	392	3	AAQ49411 Arabidops
6	1041	47.0	411	3	AAQ49410 Arabidops
7	1041	47.0	411	3	AAQ11514 Arabidops
8	757.5	34.2	379	6	AAQ38268 Rice grai
9	564.5	25.3	174	2	AAQ31934 Soybean b
10	561.5	25.3	336	3	AAQ52582 Arabidops
11	561.5	25.3	336	3	AAQ14675 Arabidops
12	561.5	25.3	346	3	AAQ14674 Arabidops
13	561.5	25.3	346	3	AAQ52581 Arabidops
14	561.5	25.3	348	3	AAQ14673 Arabidops
15	561.5	25.3	348	3	AAQ52580 Arabidops
16	561.5	25.3	348	5	ABQ92372 Herbicida
17	462.5	20.9	352	3	AAQ30070 Arabidops
18	459	20.9	352	2	AAQ31935 Wheat brl
19	457	20.6	477	4	AAQ79077 Human pro
20	457	20.6	477	5	ABQ11331 Human tra
21	457	20.6	477	7	ADQ09990 Human NOV
22	457	20.6	477	8	ADL15740 Novel hum
23	454	20.5	475	8	ADL15742 Rabbit pe
24	448	20.2	384	6	ADA54221 Human pro
25	448	20.2	468	5	AAQ22927 Human tra

26	448	20.2	471	4	AAQ27697 Human ful
27	448	20.2	475	8	ADH42321 Novel hum
28	448	20.2	509	4	AAQ27669 Human con
29	438	19.8	468	6	ABJ37928 NOXV prot
30	438	19.8	468	7	ADK51034 Human NOV
31	438	19.8	468	8	ADH42319 Novel hum
32	437	19.7	326	8	ADQ44080 Bacterial
33	425.5	19.2	469	3	AAQ76084 Murine AD
34	425.5	19.2	469	4	AAQ56023 Skin cell
35	425.5	19.2	469	5	ABQ72223 Murine pr
36	420.5	19.0	377	4	ABQ60506 Drosophi
37	420.5	19.0	508	4	ABQ22637 Novel hum
38	419.5	18.9	342	8	ADN20637 Bacterial
39	418.5	18.9	366	4	AAQ40072 Human pol
40	418.5	18.9	385	3	AAQ42329 Human ORF
41	418.5	18.9	469	3	AAQ66718 Membrane-
42	418.5	18.9	469	4	AAQ87554 Human PRO
43	418.5	18.9	469	4	AAQ65241 Human PRO
44	418.5	18.9	469	5	ABQ5879 Human sec
45	418.5	18.9	469	6	ABQ58056 Human PRO

ALIGNMENTS

RESULT 1	AAQ31936	AAQ31936 standard, protein, 289 AA.
XX	AC	AAQ31936;
XX	DT	21-DEC-1999 (first entry)
XX	DE	wheat brittle-1 partial polypeptide.
XX	KW	Brittle-1; wheat; carbohydrate; starch; transgenic plant.
XX	OS	Triticum aestivum.
XX	PN	WQ9949047-A2.
XX	PD	30-SEP-1999.
XX	PF	22-MAR-1999; 99WO-US006583.
XX	PR	26-MAR-1998; 98US-0079420P.
XX	PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	PI	Allen SM, Hitz WD, Lightner JB, Rafalaki JA;
XX	DR	WPI; 1999-591098/50.
XX	DR	N-PSDB; AAQ20025.
XX	PT	Novel genes useful in studies of carbohydrate metabolism and function in plants.
XX	PS	Claim 16; Page 42-43; 42pp; English.
XX	CC	This sequence represents a portion of wheat brittle-1, a plastidic membrane transporter involved in the transport of ADP-glucose from the cytosol to the plastid where it is used for starch biosynthesis. The sequence was deduced from an isolated partial cDNA clone (see AAQ20025).
XX	CC	The invention relates to isolated nucleic acid fragments (see AAQ31936-36) encoding plant carbohydrate biosynthetic enzymes (see AAQ31936-36) selected from 1,3-beta-D-glucan synthase and brittle-1. It also relates to the construction of a chimeric gene encoding all or a portion of a carbohydrate biosynthetic enzyme, in sense or antisense orientation, where expression of the chimeric gene results in altered levels of carbohydrate biosynthetic enzyme in a transformed host cell. The availability of nucleic acids encoding these enzymes will facilitate studies of carbohydrate metabolism and function in plants, provide genetic tools for the manipulation of these pathways, and provide a means

CC to control starch and 1,3-beta-D-glucan biosynthesis in plant cells
XX Sequence 289 AA;

Query Match 51.4%; Score 1139.5; DB 2; Length 289;
Best Local Similarity 74.5%; Pred. No. 8.9e-102;
Matches 216; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

Qy 115 RKVIGNPHLRVLSGALAGAVSRTEVPLEETIRTHLMVSGSGADSMAGVFRMIRTEGMP 174
Db 1 KIKVGNHKLKRLIGSGAGAVSRVAVPLETIRTHLMVSGNSSTEVDSIMKSGWT 59
Qy 175 GLFRGNANVNLVAPSPKAIHEFTYDTAKKYLTPPAGSPAKVPIPTPLVAGALAVASTLC 234
Db 60 GLFRGNLWNYVAVPSPKAIHEFADTAKKFLTPKSGEOKPIPIPSLVAGAFVSSSTLC 119
Qy 235 TYPEMLVKTRLTITKQVYDNLIAFVKTIVDEGGEIYRGLAPSLIGVPPAAANFYAYE 294
Db 120 TYPEMLIKTRLTIRGVYDNLIAFVKIVREGPAELYRGLTPSLIGVPPAAATNPAYD 179
Qy 295 TLKGVRRASGKEEVGNVPTLLISAGAAIATSTATPFLVAVKQMOVGAVGROVYKNVL 354
Db 180 TLKGVYKMEKTEIGNVPTLLISAGAAISTATPFLVAVKQMOVGAVGKRYVYKNVL 239
Qy 355 HAMYCIIEKSGTAGLYRGLGPSCKIKMPAGISFMCYBACCKILVDEKED 404
Db 240 HALTLTIEDEGVGLYRGLGPSCKIKLVPAGISFMCYBACCKILIEBENE 289

RESULT 2
AAG49412
ID AAG49412 standard; protein; 316 AA.

XX AAG49412;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 62508.

KW Protein identification, signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127452P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
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PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140033P.
PR 23-JUN-1999; 99US-0140035P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145088P.
PR 21-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.

PR	23.-JUN.-1999;	99US-01452218;
PR	23.-JUN.-1999;	99US-01452249;
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PR	27.-JUL.-1999;	99US-01455913;
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PR	02.-AUG.-1999;	99US-01463899;
PR	03.-AUG.-1999;	99US-01470388;
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PR	04.-AUG.-1999;	99US-01473032;
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PR	06.-AUG.-1999;	99US-01473033;
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PR	16.-AUG.-1999;	99US-01493688;
PR	17.-AUG.-1999;	99US-01491715;
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PR	26.-AUG.-1999;	99US-01508844;
PR	27.-AUG.-1999;	99US-01510652;
PR	27.-AUG.-1999;	99US-01510866;
PR	27.-AUG.-1999;	99US-01510866;
PR	30.-AUG.-1999;	99US-01513033;
PR	31.-AUG.-1999;	99US-01514387;
PR	01.-SEP.-1999;	99US-01519307;
PR	01.-SEP.-1999;	99US-01523633;
PR	07.-SEP.-1999;	99US-01530706;
PR	10.-SEP.-1999;	99US-01537588;
PR	11.-SEP.-1999;	99US-01540186;
PR	15.-SEP.-1999;	99US-01540392;
PR	16.-SEP.-1999;	99US-01547799;
PR	22.-SEP.-1999;	99US-01551392;
PR	23.-SEP.-1999;	99US-01554866;
PR	24.-SEP.-1999;	99US-01556599;
PR	28.-SEP.-1999;	99US-01564588;
PR	29.-SEP.-1999;	99US-01565666;
PR	04.-OCT.-1999;	99US-01571177;
PR	05.-OCT.-1999;	99US-01577533;
PR	06.-OCT.-1999;	99US-01578655;
PR	07.-OCT.-1999;	99US-01580239;
PR	08.-OCT.-1999;	99US-01582322;
PR	12.-OCT.-1999;	99US-01583699;
PR	13.-OCT.-1999;	99US-01592833;
PR	13.-OCT.-1999;	99US-01592844;
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PR	14.-OCT.-1999;	99US-01593310;
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PR	14.-OCT.-1999;	99US-01596477;
PR	18.-OCT.-1999;	99US-01596688;
PR	18.-OCT.-1999;	99US-01595844;
PR	21.-OCT.-1999;	99US-01607411;
PR	21.-OCT.-1999;	99US-01607677;
PR	21.-OCT.-1999;	99US-01607688;
PR	21.-OCT.-1999;	99US-01607740;
PR	21.-OCT.-1999;	99US-01608144;
PR	22.-OCT.-1999;	99US-01608155;
PR	22.-OCT.-1999;	99US-01609807;

PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 23-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161358P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161931P.
PR 29-OCT-1999; 99US-0162143P.

Query Match	47.0%;	Score 1041;	DB 3;	Length 316;
Best Local Similarity	64.9%;	Pred. No. 3.7e-92;		
Matches 203;	Conservative 47;	Mismatches 59;	Indels 4;	Gaps 2;

QY 92 EAGYGKAAOKAKKKKKQOQLSLRKVRVIGIPHLRLVLVGAIAGAVSRTPFAPLEIIRTHLM 151
| : : : : :
7 EEETVNGEERKRKKGGTL--KIKIANPSLRLLSGAVAGAVSRTVAAPLEIIRTHLM 63

Db

Qy 152 VGSAGADSNAGVFRIMIRTEGWGLFRGAVNVLRVASKAIIEFTYDPAKTYLTPEAGE 211
 Db 64 VG-SGANSSTEVSDDIMKHEGWGLFRGNLVNIVRPARAVELVFVEIVNKKLSPPHQ 122

Oy 212 PAKPPIPRVLVAGLAVASTLTCTYPMELVKTLTIKDVVDNLLHAFAKIIVDEGPGL 271
 : :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 123 ESKIPFASLIACGVSQTLTYPLELVKLITIQGVKKGFDAFLIKIRREGPTIL 162

Figure S8. Multiple sequence alignment of the protein sequences from different species.

Qy 272 YRGAPSLIGVPPAAANFYAYETLRGVRRPAAQKEEKNPTLLIGSAAGAASTATPP 331
Db 183 YRGAPSLIGVPPAATNFYAYDSLRKAYRFSKQEKGNIEITLLIGSLAALSTATPP 242

Db

332 LEVARKQGVGAVGROYKKNVTHAMCYCLBKSGTAGIYRGLGSSCIKIMPAAGISFMCY 391

332 LEVARKQGVGAVGROYKKNVTHAMCYCLBKSGTAGIYRGLGSSCIKIMPAAGISFMCY 391

243 LEVARKQGVGAVGSRVVYKNNMLHALVTLLEHGIIIGWYKGLGSPSCIKLVPAAGISFMCY 302

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QY      392 EACKILVDEKED 404
          |||||:::
Db      303 EACKILIENNOE 315
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RESULT 3
AAG11516
ID AAG11516 standard: protein: 316 AA.

AA AAG11516;
AC
XX
DT 17-OCT-2000 (first entry)

Accession	Protein identification; signal transduction pathway; me	Arabidopsis thaliana protein fragment SEQ ID NO: 10261..
AA010000	Protein identification; signal transduction pathway; me	Arabidopsis thaliana protein fragment SEQ ID NO: 10261..
DE010000	Protein identification; signal transduction pathway; me	Arabidopsis thaliana protein fragment SEQ ID NO: 10261..
XX010000	Protein identification; signal transduction pathway; me	Arabidopsis thaliana protein fragment SEQ ID NO: 10261..
KM010000	Protein identification; signal transduction pathway; me	Arabidopsis thaliana protein fragment SEQ ID NO: 10261..

OS	<i>Arabidopsis thaliana</i> .
XX	
KM	termination sequence.
AN	hyperabundant body / generate mapping / gene expression control / promoter

PN	EP1033405-A2.
XX	
PD	06-SEP-2000.

PF	25-FEB-2000; 2000EP-00301439.
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PR	25-FEB-1999; 99US-0121825P.

PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	09-MAR-1999;	99US-0123548P.

PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.

	Query Match	47.0%; Score 1041; DB 3; Length 316;
	Best Local Similarity	64.9%; Pred. No. 3,7e-92;
	Matches 203; Conservative	47; Mismatches 59; Indels 4; Gaps 2;
PR	22-OCT-1999; 99US-0160981P.	
PR	22-OCT-1999; 99US-0160989P.	
PR	25-OCT-1999; 99US-0161404P.	
PR	25-OCT-1999; 99US-0161405P.	
PR	25-OCT-1999; 99US-0161406P.	
PR	26-OCT-1999; 99US-0161359P.	
PR	26-OCT-1999; 99US-0161360P.	
PR	26-OCT-1999; 99US-0161361P.	
PR	28-OCT-1999; 99US-0161920P.	
PR	28-OCT-1999; 99US-0161922P.	
PR	28-OCT-1999; 99US-0161933P.	
PR	29-OCT-1999; 99US-0162142P.	
QY	EAGYQKQKAKKAKKQQLSLKRVKIGNPILRLVSGAIGAVSRFPVAPLETIRTHLM	151
DB	7 EEEVNVGKKRRKKKKGGULT--KIKIANPSLRLLSGAVAGASRTVAPLETIRTHLM	63
QY	152 VGSSGADSMAGVFRMINRTGEMPGELFRGNAVNVRVAPSKAIEHFYDTAKKYLTPEAGE	211
DB	64 VG-SGGNSSTVFSDIMKHESMTGLFRGNLVNVRVAPARAVELFVETVKKLSPRNGQ	122
QY	212 PAKYPIPTPLVAGALAGVASTLCTCYPEMLVYTRLLTIKDYVDNLLHAFVKIVRDEGPEL	271
DB	123 ESKTPIPSALLAGACAGVSQLTLTYPLVTRLLTIQGVYKGFADFALKIIRREGPTL	182
QY	272 YRGLAPSLIGVPPPAANFVYETLRGVRRPASKEVGNVPTLLIGSAAQALSTATP	331
DB	183 YRGLAPSLIGVPPPAATVTFAYDRLKRVRSFSKOEKIGIETLLIGSLAGALSTATP	242
QY	332 LEVARKQOVGAVGROYKKNVLAHMYCIIEKEGTAGLYRGLGPSCTIKMPAAGISFWCY	391
DB	243 LEVARKKHQVGAVSGRVVYKNNLHALVTLLIEHGILGMYKGLGPSCLTVPAAGISFWCY	302
QY	392 EACKKILVDEKED 404	
DB	303 EACKKILLENNGE 315	
RESULT 3		
AA01516		
ID	AA01516 standard; protein; 316 AA.	
XX		
AC	AA01516;	
XX		
DT	17-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 10261.	
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
XX	termination sequence.	
OS	Arabidopsis thaliana.	
XX		
EN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-00301439.	
XX		
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PR	25-FEB-1999; 99US-0121825P.	
PR	05-MAR-1999; 99US-0123180P.	
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PR	25-MAR-1999; 99US-0126264P.	
PR	29-MAR-1999; 99US-0126785P.	
PR	01-APR-1999; 99US-0127462P.	
PR	06-APR-1999; 99US-0128234P.	
PR	08-APR-1999; 99US-0128714P.	

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PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130049P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
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PR 22-OCT-1999; 99US-0160980P.
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PR 25-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 47.0%; Score 1041; DB 3; Length 316;
Best Local Similarity 64.9%; Pred. No. 3.7e-92;
Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

QY 92 EAGVQAKQAKAKKQOLSLRKVRKIGNPHLRVLSGAIAGAVSTFPVAPLETITHTM 151
DB 7 EEEVNVGEGKRRKKKGGTLT---KIKIAPSLRKLISGAVAGVSTVVAPELTITHTM 63
QY 152 VSSGSGDSVAGVFRWIMRTGEMGLFRGNVNVLRVAPSKALEHFTYDTAKKYLTEAGE 211
DB 64 VG--SGNSSTVEFSDIMKEHGWGLFRGNLVNVIRVAPARAVELFVFETVKKLSPHQ 122
QY 212 PAKVPPTPLVAGALAGVASTLCTVPMELVKTRLTEKVDNLMAFPKIVRDEPGRL 271
DB 123 ESKIRPASPGLAGACGVSTLTLYPLELVKTRLTIQRGVYKGIIDPAFKIRBEGPTL 182
QY 272 YGLAPSLIGVVPYAAAFAYETTLRGVYRRASGKEEVGNVPTLISGAAGAIATATPP 331
DB 183 YGLAPSLIGVVPYAAAFAYETTLRGVYRRASGKEEVGNVPTLISGAAGAIATATPP 242
QY 332 LEVARKQOVGAVGGRQVYKVVLMVAMVCTLEKEGTAGLYRGGLGPGSCIKLMPAGISFMCY 391
DB 243 LEVARKQOVGAVGGRVYKVVLMVAMVCTLEHEGLIGVYKGLGPGSCIKLVPAAGISFMCY 302
QY 392 EACKKILVDEKED 404
DB 303 EACKKILVDEKED 315

RESULT 4
AAG1515
ID AAG1515 standard; protein, 392 AA.

AC AAG1515;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 10260.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX

PD, 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
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XX 28-APR-1999; 99US-0131449P.
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XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
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XX 07-JUN-1999; 99US-0137724P.
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QY 152 VGSSGADSNAGVPRWIMRTIEGMPGLFRGNANVTLRVAPSKAIEMFTYDRAKKYLTPEAGE 211
DB 140 VG-SGNSSSTFEVSDIMKHKGWGLFRGNLNVNIRVAPAVBELFVEETVNNKLSPEHQ 198
QY 212 PAKVPIPTPLVAGALGVASTLCTYPMELVKTRLTTEKDYVDLILAFVKIVRDESGEL 271
DB 199 ESKIPPIPASILAACGVSQTLTLPBELVKITLTIQRGVYKQIPDAFLKIIEBGPTEL 258
QY 272 YRGLAPSLIGVVEYAANFAVETLRGVYRRASGKEVEGNVPTLLIGSAGAIATATFP 331
DB 259 YRGLAPSLIGVVEYAANTVYAYDSLKAYRSPSKOEKIGNIEFTLLIGSLAGALSTATFP 318
QY 332 LEVARKOMQVAGVGGQVYNNVILHMYCIIEKKGITGLIRGLGSPSCIKLMPAGISPMCY 391
DB 319 LEVARKMQVGAIVSGVYVYNNMLHALVTILIEHGIILGWYKGLSPSCIKLWPAAGISPMCY 378
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PF	25-FEB-2000; 2000EP-00301439.		
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AC
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DT 17-OCT-2000 (first entry)
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
OS Arabidopsis thaliana.
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KW grain quality; nutritional content; plant yield; BT1; plant.

Oryza sativa.

PN W02003048319-A2.

PD 12-JUN-2003.

PF 27-NOV-2002; 2002WO-US038359.

PR 30-NOV-2001; 2001US-0334501P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Sainz MB, Salmeron J, Welzlo L;

DR WPI; 2003-505288/47.

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CC proteins for abiotic stress tolerance, enhanced pathogen or disease

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KM Protein identification; signal transduction pathway; metabolic pathway;
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KM termination sequence.

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XX
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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1625	100.0	1625	9	US-09-796-766-17
2	1625	100.0	1625	17	US-10-659-199-17
3	678	41.7	1715	18	US-10-437-963-47977
4	674	41.5	1588	17	US-10-425-114-8901
5	673.4	41.4	675	17	US-10-260-238-3967
6	672.8	41.4	1578	17	US-10-425-114-16127
7	672.8	41.4	1666	17	US-10-425-114-25407
8	672.6	41.4	1213	17	US-10-260-238-1023
9	549	33.8	698	17	US-10-260-238-2898
10	539.4	33.2	640	17	US-10-260-238-3968
11	511	31.4	661	17	US-10-260-238-3969

12	482.2	29.7	1951	18	US-10-437-963-44128	Sequence 44128, A
13	477.2	29.4	1516	17	US-10-425-114-30842	Sequence 30842, A
14	477.2	29.4	1732	17	US-10-425-114-27699	Sequence 27699, A
15	477.2	29.4	2090	18	US-10-425-115-13272	Sequence 13272, A
16	475.6	29.3	1817	17	US-10-425-114-793	Sequence 793, App
17	440.4	27.1	1056	17	US-10-260-238-3974	Sequence 3974, Ap
18	435	26.8	1816	18	US-10-437-963-19933	Sequence 19933, A
19	424.4	26.1	1988	17	US-10-425-114-28457	Sequence 28457, A
20	424.4	26.1	2166	18	US-10-425-115-60739	Sequence 60739, A
21	400.4	24.6	787	18	US-10-437-963-47978	Sequence 47978, A
22	400.2	24.6	1267	9	US-09-796-766-19	Sequence 19, Appl
23	400.2	24.6	1267	17	US-10-659-199-19	Sequence 19, Appl
24	397.6	24.5	1140	18	US-10-491-733-25	Sequence 25, Appl
25	392.6	24.2	449	9	US-09-796-766-15	Sequence 15, Appl
26	392.6	24.2	449	17	US-10-659-199-15	Sequence 15, Appl
27	374.2	23.0	632	18	US-10-437-963-47980	Sequence 47980, A
28	361.6	22.3	1099	17	US-10-260-238-3975	Sequence 3975, Ap
29	340.2	20.9	1723	17	US-10-424-599-142274	Sequence 142274, A
30	303	18.6	1089	9	US-09-796-766-13	Sequence 13, Appl
31	303	18.6	1089	17	US-10-659-199-13	Sequence 13, Appl
32	256.8	15.8	653	17	US-10-260-238-3973	Sequence 3973, Ap
33	255.4	15.7	2772	18	US-10-425-115-109610	Sequence 109610, A
34	254.8	15.7	1068	17	US-10-424-599-122492	Sequence 122492, A
35	249.8	15.4	606	18	US-10-767-701-15885	Sequence 15885, A
36	222.4	13.7	654	17	US-10-260-238-5581	Sequence 5581, A
37	191.6	11.8	670	18	US-10-767-701-6466	Sequence 6466, Ap
38	184.2	11.3	506	18	US-10-437-963-82850	Sequence 82850, A
39	169.2	10.4	1166	17	US-10-424-599-99067	Sequence 99067, A
40	167.8	10.3	481	17	US-10-425-114-15391	Sequence 15391, A
41	150.2	9.2	471	18	US-10-425-115-77056	Sequence 77056, A
42	149.8	9.2	233	18	US-10-425-115-51603	Sequence 51603, A
43	144	8.9	1062	9	US-09-796-766-3	Sequence 3, Appl1
44	144	8.9	1062	17	US-10-659-199-3	Sequence 3, Appl1
45	136.8	8.4	2107	18	US-10-425-115-10510	Sequence 10510, A

ALIGNMENTS

RESULT 1
US-09-796-766-17
Sequence 17, Application US/09796766
Patent No. US20010047523a1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: B1157 US CIP
CURRENT APPLICATION NUMBER: US/09/796, 766
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 1625
TYPE: DNA
ORGANISM: Trilicium aestivum
US-09-796-766-17

Query Match 100.0%; Score 1625; DB 9; Length 1625;
Best local similarity 100.0%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCACGTGAGGAGTGAAGAACTCTAGCAGGCGACGTATCAGTTCTGTCT 60
Db 1 GGCACGTGAGGAGTGAAGAACTCTAGCAGGCGACGTATCAGTTCTGTCT 60

QY 61 TGTCTCTGAGATGCGCGCGCAATGCGCGAGCAACATGATGTGATCCAAAGAACACCGC 120
DB 61 TGTCTCTCTGAGATGCGCGCGCAATGCGCGAGCAACATGATGTGATCCAAAGAACACCGC 120
QY 121 GCGTCGCTGCTGATGGAAGAAAGAACTGATTTATGCGCGCGCGCGCGCGCGCGCGCGCTT 180
DB 121 GCGTCGCTGCTGATGGAAGAAAGAACTGATTTATGCGCGCGCGCGCGCGCGCGCGCGCTT 180
QY 181 CTTTGAGACTCGACGCGCGAGCTTCAGAGCTTGTGACTTCCACGAGGAGCTCTGTTCCGC 240
DB 181 CTTTGAGACTCGACGCGCGAGCTTCAGAGCTTGTGACTTCCACGAGGAGCTCTGTTCCGC 240
QY 241 AGCGTGGAGCTCAGCTGTGTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 300
DB 241 AGCGTGGAGCTCAGCTGTGTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 300
QY 301 GCTCGGCGCGCGCGAGAGCTGCGACACGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 GCTCGGCGCGCGCGAGAGCTGCGACACGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 AAGGCGCGAGAGCG 420
DB 361 AAGGCGCGAGAGCG 420
QY 421 AAGATCGGCAACCGCGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 480
DB 421 AAGATCGGCAACCGCGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 480
QY 481 AAGATCTTCTGCTGCG 540
DB 481 AAGATCTTCTGCTGCG 540
QY 541 GCGGAGCTGAGCG 600
DB 541 GCGGAGCTGAGCG 600
QY 601 TTCCGCGGCAACCGCGTCAACGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 TTCCGCGGCAACCGCGTCAACGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 ACTTACGACAGCGCGAGAAAGTACTTGAACCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 661 ACTTACGACAGCGCGAGAAAGTACTTGAACCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 ATCCCGAGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 721 ATCCCGAGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 CCGATGAGCTGCTCAAGACCGCTCTCAACATCGAAGAGAGAGCTGTACGACACCTCTC 840
DB 781 CCGATGAGCTGCTCAAGACCGCTCTCAACATCGAAGAGAGAGCTGTACGACACCTCTC 840
QY 841 CACGCGTTCGTCAGAGTGTGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
DB 841 CACGCGTTCGTCAGAGTGTGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 901 CCGAGCGCTGATCGGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
DB 901 CCGAGCGCTGATCGGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 961 CCGGCGCTGTACCG 1020
DB 961 CCGGCGCTGTACCG 1020
QY 1021 ATCGGCGTCCG 1080
DB 1021 ATCGGCGTCCG 1080
QY 1081 AAGCAGATGCAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1081 AAGCAGATGCAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1141 ATGTACTCATCTCTGAGAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200

DB 1141 ATGTACTCATCTCTGAGAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1201 TGCATCAAGCTCATGCG 1260
DB 1201 TGCATCAAGCTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1261 ATACTTGTGAG 1320
DB 1261 ATACTTGTGAG 1320
QY 1321 GGAAGGAG 1380
DB 1321 GGAAGGAG 1380
QY 1381 TGAAGCATTTATGAG 1440
DB 1381 TGAAGCATTTATGAG 1440
QY 1441 GTAGAGCTTATGAG 1500
DB 1441 GTAGAGCTTATGAG 1500
QY 1501 TTTGTTAG 1560
DB 1501 TTTGTTAG 1560
QY 1561 GTATCAATTCATTAAG 1620
DB 1561 GTATCAATTCATTAAG 1620
QY 1621 AAAA 1625
DB 1621 AAAA 1625

RESULT 2
US-10-659-199-17
Sequence 17, Application US/10659199
Publication No. US20040038287A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafaleki, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: B1157 US CIP
CURRENT APPLICATION NUMBER: US/10/659,199
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US/09/796,766
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 1625
TYPE: DNA
ORGANISM: Trilicium aestivum
US-10-659-199-17

Query Match 100.0%; Score 1625; DB 17; Length 1625;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCAGTGAAG 60
DB 1 GCGCAGTGAAG 60
QY 61 TGTCTCTCTGAGATGCGCGCGCAATGCGCGAGCAACATGATGTGATCCAAAGAACACCGC 120

Db 61 TGGTCTCCAGATGCGGCGGCATGCGCGCGACGACAAATGATGACCAAGAACACGCG 120
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Db 121 GCGTCGCTGCTCATGAGCAAGAAAGAACTGGTTATTTGCGCGCGGCTTGAAGTCCGCTTC 180
Qy 181 CCTTGGAGCTCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 CCTTGGAGCTCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
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Db 241 AGGCTGGAGCTCAAGCTGTCTCCACGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Qy 301 GCTCGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
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Db 481 AGGACTTTCGTCG 540
Qy 541 GCGGACTCCATGCG 600
Db 541 GCGGACTCCATGCG 600
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Qy 721 ATCCGCGCGCGCTCG 780
Db 721 ATCCGCGCGCGCTCG 780
Qy 781 CCCGATGAGCTGTCAAGACCCGCTCTCAACCATCGAGAGGACGCTGTACGACCACTCTCTC 840
Db 781 CCCGATGAGCTGTCAAGACCCGCTCTCAACCATCGAGAGGACGCTGTACGACCACTCTCTC 840
Qy 841 CACGCGCTTGTCAAGATCGTCCG 900
Db 841 CACGCGCTTGTCAAGATCGTCCG 900
Qy 901 CCGAGCGTATCG 960
Db 901 CCGAGCGTATCG 960
Qy 961 CCGCGCGTGTACCG 1020
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Db 1021 ATCGGAGTCCG 1080
Qy 1081 AAGCAGATGAGTGGGCG 1140
Db 1081 AAGCAGATGAGTGGGCG 1140
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Db 1141 ATGTACTGATCTCTCGAGAGAGGACCGCGCGCGCTCTACCGCGCGCGCTCGCGCGCGCGCGCG 1200

Db 1141 ATGTACTGATCTCTCGAGAGAGGACCGCGCGCGCTCTACCGCGCGCGCTCGCGCGCGCGCGCG 1200
Qy 1201 TGCATAGAGCTCATGCG 1260
Db 1201 TGCATAGAGCTCATGCG 1260
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Db 1261 ATACTTGTGCGACGAGAAAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Qy 1321 GGAAG 1380
Db 1321 GGAAG 1380
Qy 1381 TGAAGCATTAATGCTGACCG 1440
Db 1381 TGAAGCATTAATGCTGACCG 1440
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Db 1441 GTAGAGCTTAATGCGAGTGAATCTAAGCTGAGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
Qy 1501 TTTGTTCAAGGAAACATGCTCCGTTTCAATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1560
Db 1501 TTTGTTCAAGGAAACATGCTCCGTTTCAATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1560
Qy 1561 GTATCAATTCATTAAGAGAGAGTCACTTTTGAACCTTCAAAAAAATTTTGAAGT 1620
Db 1561 GTATCAATTCATTAAGAGAGAGTCACTTTTGAACCTTCAAAAAAATTTTGAAGT 1620
Qy 1621 AAAAA 1625
Db 1621 AAAAA 1625

RESULT 3
US-10-437-963-47977/c
Sequence 47977, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukhariyov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 47977
LENGTH: 1715
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1715)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_50695C.1
US-10-437-963-47977

Query Match 41.7%; Score 678; DB 18; Length 1715;
Best local similarity 66.9%; Pred. No. 2, 1e-174;
Matches 1087; Conservative 0; Mismatches 470; Indels 67; Gaps 6;
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Db 1592 CTCCTAGGAGTCAAGAGAGTATTATTGTTGATGATGATGCGCGCGCAATGCG 1533

90 CGCGACGAATGTGACCAAGAACACCGGCTCGTCA---TGACAAAGAA 146
1532 GGTACGACGATGTGACGAGAAACACCGCTGGCGGCGCGGCTGCTGGA 1473
147 CTGTTATTTGGCGCGGCTCGTGAAGTGCCTTCCCTTGAAGCTCGACGCCAGTCCAG 206
1472 CAGGAAGGGGTGTGTTGCTCCCGAGAGTGTCTTCCCGTGAAGCTCGGTGAAGGGAGCG 1413
207 GAGCTTGAATTTCCACGACGAGGCTCTTTCGACGCTGGAAGCTCAAGCTGTCCACGG 266
1412 CATCAACGACGACGACGAAGATTGAGATTCTCGCGACGAGCGGCGCGCTGTT 1353
267 CGCCCGCGCGGTAAGCGCGGACGA---TGACGGGAAGGCTGGGCGCGCGACGAGTGGC 323
1352 CGCAGCGCTCGGCTCAAGCTTGGCTGTGCGCGAAGGGCGGGAACAACTCGACGTGCG 1293
324 ACACGAGCTCGACGCGC-----GGCGAAGCGGCGCTCGAAGAGGCCAGAAAGGC 374
1292 GCGGAGCTCGCGCGCGCGGAGGCGCGGAGAGGCGGGAAGAGGACAGGCGACGAA 1233
375 GAAAAAGGCCAAAAAGACGACGCTGATCTGAGAGGTGAGGTCAAGATCGGCAACC 434
1232 GATGAAGGGCGCGCGGCTGTGCTGTGAGGAAGGTGAGGTGAAGATCGGAAACC 1173
435 GCACCTGCGGCGGCTGCTGACGCGGCGCATGCGCGGCGCGTGTGAGAGCTTTGATGCG 494
1172 GACCTTTCGCGGCTGTGAGCGGCGCATGCGCGGCGCGTGTGCGCACCTTGTGAGC 1113
495 GCCACTGAGAGCGATCAGACGACCTGATGTGGGAGCTCGGCGCGCATCCATGCG 554
1112 GCGCGTGAAGACATCCGACCCCATCTCATGTTGCGGACGCTGCGGCGCGCTCCATGCG 1053
555 CGGGGTTTTCCGTTGATCATGCGGAGCGGAGGCTGCGGCGCTTTCGCGGCAAGC 614
1052 CGAGGTCCTTCGCTGATCATGCGGACCGAGGCTGAGCCGCGCTTTCGCGGCAAGC 993
615 CGTCAAGTCTCGCGGCTCGGCGCAAGAGCCATCGACACTTACGACAGCGC 674
992 CGTCAAC-----GCAATTCACCTACGACAGCGC 965
675 GAAGAAGTACTGACCCCGGAGCGCGGACGACGACCAAGGTCCCATCCCGACGCGCT 734
964 CAAGAAGTACTTACCCCGGAGGAGCGGAGCCTGCAAGATCCCATCCCGTCCCT 905
735 CGTGGCGGAGCGCTCGCGGAGTGGCTCAACCTGTGCACTTATCCATGAGACTGCT 794
904 CGTGGCGGCGCGCTCGCGGAGTGGCTCAACCTGTGCACTTATCCATGAGACTGCT 845
795 CAAGACCGGCTCAACATCGAAGAGGAGTGTAGCAACCGCTCCGAGGCTGCTGCA 854
844 CAAGACCGGCTCAACATCGAAGAGGAGTGTAGCAACCGCTCCGAGGCTGCTGCA 785
855 GATCGTGGCGACGAAGGCGCGGAGAGCTGTACCGCGGCTGAGCGCGGACCTGATCG 914
784 GATCGTGGGAGAGGCGCGGAGAGCTGTACCGCGGCTGAGCGCGGACCTGATCG 725
915 CGTGTGCTGTAACGCGGCGGACCACTTCTTACGACGAGGCTGCGGCGGCTGTAACG 974
724 CGTGTGCTGTAACGCGGCGGACCACTTCTTACGACGAGGCTGCGGCGGCTGTAACG 665
975 CGGCGCTGCGGGAAGAGAGGAGTGGGCAAGTCCCGACGCTGATCGGCTCGGCGG 1034
664 CGGCGCGACGCGGCGCGGACGCTGCGCGGCGGCGGCTGCTCATCGGCTCGGCGG 605
1035 GGGCGCATAGCAGACGACGCTTCCGCTGAGAGTGGCGCGGAGAGCATGACAGT 1094
604 GGGCGCATAGCAGACGACGCTTCCGCTGAGAGTGGCGCGGAGAGCATGACAGT 545
1095 GGGCGCTGAGCGGAGGAGGAGTGTACAGAAAGTGTGCAAGCATGTACTGATCT 1154
544 CGGCGCGCTGCGGCGGCGGAGGTGTACCGGCAAGTGTCCACGCGCATGTAAGTCTGATCT 485

QY 1155 CGAAGAGAGGACCGCGCGGCTTAACCGCGGCTTCGCGCCAGCTGATCAAGCTCAT 1214
DB 484 CGCGGAGGAGGCGCGCGGCTTACCGCGGCTTCGCGCCAGCTGATCAAGCTCAT 425
QY 1215 GCCCGCGCGGCGGATCTCTTCAATGTCTACGAGGCTTGAAGATTAATTTGCGACGA 1274
DB 424 GCCCGCGCGGCGGATCTCTTCAATGTCTACGAGGCTTGAAGATTAATTTGCGACGA 365
QY 1275 GAAAG-----AAGACGCGCGCGCGCGGCGCGGCGCGGCGCGGCGGCGGCGGCGG 1322
DB 364 GAGAGCGGCGCGCGGAGCTGAGAGCGGAGTCCGCGGAGAGATCAAGAGAGAGTTCGCTG 305
QY 1323 ACAAGCAGAGACGACGCGCGCGCAAGACCTGAACGATGCGCATGAATCTAGATG 1382
DB 304 AAGTGTGTTGGGCTCGCGCGCGCGGAGAGATGTGTGCTGATGTCAGTGGGTGATG 245
QY 1383 -----AAGCATTAATGTGACCGCTCAAAATCAAGAAATATGCGTGAATTTT 1434
DB 244 ATGGAAGCATGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTTCGCTG 185
QY 1435 TGAAGTGAAGCTTAATGCGATTAATCTTAAGCTGGAAGTGGCGCTTGAAGTTGAA 1494
DB 184 TGCTGTGTTTGAAGTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 125
QY 1495 TTTGTTTGTTCAGGAGCATGCTCGTTTCAAGTATGCGGATGATGATGATGATGATGATG 1554
DB 124 TATGTTGTGTTTCAATGAAGTATGATGATGATGATGATGATGATGATGATGATGAT 65
QY 1555 CTTTCTGTAATCAATTAAGAGAGAGTCACTTTGAGACTTCAAAAAA 1614
DB 64 GCATTTCAAGTTGTTTCAATTAAGAGAGTCACTTTGAGACTTCAAAAAA 5
QY 1615 AAAA 1618
DB 4 AAAA 1

RESULT 4
US-10-425-114-8901
Sequence 8901, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kowalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8901
LENGTH: 1588
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700802849_FLI
US-10-425-114-8901

Query Match 41.5%; Score 674; DB 17; Length 1588;
Best Local Similarity 84.6%; Pred. No. 2.6e-173;
Matches 772; Conservative 0; Mismatches 132; Indels 9; Gaps 1;

QY 395 AGCTAGCTGAGAGAGTGAAGTCAAGATCGGCAACCGGACCTGCGCGGCTGATCA 454
DB 462 ATCTGACCTGAAGAGAGTCAAGTCAAGATCGGCAACCGGACCTGCGCGGCTGATCA 521
QY 455 GCGGCGCATGCGCGGCGCGGCTGTGAGAGCTTTCGTGCGGCACTGAGAGCATGACGA 514
DB 522 GCGGCGCATGCGCGGCGCGGCTGTGAGAGCTTTCGTGCGGCACTGAGAGCATGACGA 581

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Qy 515 CGACCTGATGTGGAGAGTCCGCGCCGACTTCATGCGGGGTTTCCGGTAGTCA 574
    |||||
Db 582 CGACTTGAATGTGCGAGCATCGGCTTCACTTCATGCGGGGTTTCAATGATCA 641
    |||||
Qy 575 TCGGAGCGAGGGGTGGCCCGGCTCTTCCGCGCAACGCGCTCAACGCTCCGCGTCG 634
    |||||
Db 642 TGCAGAACGAAAGGTGGACCGGCTGTTCCGGCGCAACGCGCTCAACGCTCCGCGTCG 701
    |||||
Qy 635 CGCCAGCAAGCGGCTTCGAGCACTTCACTTACGACAGCGGAAAGTAATCTGACCCCGG 694
    |||||
Db 702 CTCGAGCAAGCGGCTTCGAGCACTTCACTTACGACAGCGGAAAGTAATCTGACCCCGG 761
    |||||
Qy 695 AGGCGGCGAGCGAGCGGCTTCGAGCACTTCACTTACGAGCCGCTGTCGCGGAGCGGTCGCG 754
    |||||
Db 762 AGGCGGCGAGCGGCGGCAAGTCCGATCCGCTGCTGCTGCGGAGCGCTTCGAGCGG 821
    |||||
Qy 755 GAGTGGCGTCAACCCCTGTGACCTTATCCATGAGAGCTGTCAGAACCCGCTGTCACATCG 814
    |||||
Db 822 GATTGCGCTCAACCTTGTGACCTTATCCGATGAGAGCTGTCAGAACCCGCTGTCACATCG 881
    |||||
Qy 815 AGAAGAGCTGTACGACAACTCTCTGAGCGCTTCTGCAAGATGTCGCGAGCAAGAGCC 874
    |||||
Db 882 AGAAGAGCTGTACGACAACTCTCTGAGCGCTTCTGCAAGATGTCGCGAGCAAGAGCC 941
    |||||
Qy 875 CGGGGAGCTGTACCGGCGGCTGCGCGCGGAGCGGCTGATCGGCGGCTGACGCGCGCG 934
    |||||
Db 942 CGTGGAGCTGTACCGGCGGCTGAGCACTTATGAGAGCTGTCGCGGAGCGGCTGTCGCG 1001
    |||||
Qy 935 CCAACTTCTACGCGCTACGAGACGCTGCGCGGCTGTACCGCGCGCTGCGCGG----- 987
    |||||
Db 1002 GTAACTTCTACGCGCTACGAGACGCTGAGAGGCTGTACCGCGCGCTGCGCGGCGGCTG 1061
    |||||
Qy 988 --AAAAGAGAGTGGGAGCACTGCTCCGAGCTGCTGATCGGCTGCGCGCGGCGCGCTAG 1045
    |||||
Db 1062 CCGGCGGAGAGTGGGAGCACTGCTCCGAGCTGCTGATCGGCTGCGCGCGGCGCGCTAG 1121
    |||||
Qy 1046 CAGACGCGGAGAGTGGGAGCACTGCTCCGAGCTGCTGATCGGCTGCGCGCGGCGCGCTAG 1105
    |||||
Db 1122 CCGAGCTGCGGAGAGTGGGAGCACTGCTCCGAGCTGCTGATCGGCTGCGCGCGGCGCGCTAG 1181
    |||||
Qy 1106 GCGGAGAGAGTGTACGAGAACTGCTGAGCACTGCTGATCGGCTGCGCGCGGCGCGCTAG 1165
    |||||
Db 1182 GCGGAGAGAGTGTACGAGAACTGCTGAGCACTGCTGATCGGCTGCGCGCGGCGCGCTAG 1241
    |||||
Qy 1166 GCAACCGCGGAGCTGTACGAGAGTGTGCGGCGGCGGCTGAGCACTGAGCTGAGCTGAG 1225
    |||||
Db 1242 GCGCGGCGGAGCTGTACGAGAGTGTGCGGCGGCGGCTGAGCACTGAGCTGAGCTGAG 1301
    |||||
Qy 1226 GCATCTCTTCACTGTGTACGAGAGCTGCGGAGAGTAATCTTGTGAGAGAGAGAGAG 1285
    |||||
Db 1302 GCATCTCTTCACTGTGTGTACGAGAGCTGCGGAGAGTAATCTTGTGAGAGAGAGAG 1361
    |||||
Qy 1286 GCGGCGGCGGCGGAG 1298
    |||||
Db 1362 AGGAGAGAGAGAGAG 1374
    |||||

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RESULT 5
US-10-260-238-3967
; Sequence 3967, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moushaher, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell

```

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; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 3967
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-10-260-238-3967

```

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Query Match 41.4%; Score 673.4; DB 17; Length 675;
Best Local Similarity 99.9%; Pred. No. 2,7e-173;
Matches 674; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 912 CGGCGTGTGCGCGTACCGCGCGCACTTCTACGCGCTACGAGACGCTGCGCGGCTGT 971
    |||||
Db 1 CGGCGTGTGCGCGTACCGCGCGCACTTCTACGCGCTACGAGACGCTGCGCGGCTGT 60
    |||||
Qy 972 CCGCGCGCGCTCGGAGAGAGAGTGGGCACTTCCGAGCGCTGCTGATCGGCTCCG 1031
    |||||
Db 61 CCGCGCGCGCTCGGAGAGAGAGTGGGCACTTCCGAGCGCTGCTGATCGGCTCCG 120
    |||||
Qy 1032 GCGGCGGCGCATATGCGAGCACTGCGCGCACTTCCGCTGAGAGTGGGCGGAGAGATGCA 1091
    |||||
Db 121 GCGGCGGCGCATATGCGAGCACTGCGCGCACTTCCGCTGAGAGTGGGCGGAGAGATGCA 180
    |||||
Qy 1092 GGTGGGCGCGTGGGAGGAGGAGGAGGAGGAGTGTACAAAGAGTGTGTCAGCGCACTGATGAT 1151
    |||||
Db 181 GGTGGGCGCGTGGGAGGAGGAGGAGGAGGAGTGTACAAAGAGTGTGTCAGCGCACTGATGAT 240
    |||||
Qy 1152 CCTCGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1211
    |||||
Db 241 CCTCGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
    |||||
Qy 1212 CATGCGGCGCGCGGAGTCTCTTCACTGTGTACGAGAGGCTGCAAGAGTACTTGTGCA 1271
    |||||
Db 301 CATGCGGCGCGCGGAGTCTCTTCACTGTGTACGAGAGGCTGCAAGAGTACTTGTGCA 360
    |||||
Qy 1272 CGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1331
    |||||
Db 361 CGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
    |||||
Qy 1332 AGGACAGGCGGCGCGCAAGAGCTGCAACGAGTGTGCGGCACTGATGATGAGCACTTAT 1391
    |||||
Db 421 AGGACAGGCGGCGCGCAAGAGCTGCAACGAGTGTGCGGCACTGATGATGAGCACTTAT 480
    |||||
Qy 1392 GGTGACCGGTCAAAATGAGAGAAATGCGTGAATTTTGAAGTGTAGAGCTAT 1451
    |||||
Db 481 GGTGACCGGTCAAAATGAGAGAAATGCGTGAATTTTGAAGTGTAGAGCTAT 540
    |||||
Qy 1452 TCGATTGATCTTAAGTGTAGAGTGGCGCTTGAAGTGTGAATTTGTTTTGTTCAGAG 1511
    |||||
Db 541 TCGATTGATCTTAAGTGTAGAGTGGCGCTTGAAGTGTGAATTTGTTTTGTTCAGAG 600
    |||||
Qy 1512 AACATGCTCGTTTCACTAATGCGTGAATGTTATGAGCACTTCTGTATCAATTC 1571
    |||||
Db 601 AACATGCTCGTTTCACTAATGCGTGAATGTTATGAGCACTTCTGTATCAATTC 660
    |||||
Qy 1572 AATAAGAGAGAGTTC 1586
    |||||
Db 661 AATAAGAGAGAGTTC 675
    |||||

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RESULT 6
US-10-425-114-16127

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```
; Sequence 16127, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 16127
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-107-H7_FLI
US-10-425-114-16127

Query Match      41.4%; Score 672.8; DB 17; Length 1578;
Best Local Similarity 84.4%; Pred. No. 5.4e-173;
Matches 771; Conservative 0; Mismatches 133; Indels 9; Gaps 1;
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Db      1115  CAACTCGGCGACGTTCCGCTAGAGTGGCCCGCAAGCAAGATGACGTGAGCGCTGTG 1174
Oy      1106  GCGGAGGACAGTGTATCAAGAACGTGTGACGCCCATGTATGATCTCTGAGAGGAGG 1165
Db      1175  GCGGAGGACAGTGTATCAAGAACGTCTCCACCTATCTATGATCTTCAAGAGGAGG 1234
Oy      1166  GCACCGCGGAGCTTCAACGCGGGGTGCGCCCAAGCTGATCAAGTATGCGCGCGCG 1225
Db      1235  GCGCGGCGGCTGTATCCGAGGTCTCGCCCTGATGATCAAGCTATGCGCGCGCG 1294
Oy      1226  GCATCTCTTCAATGTCTAGAGCGCTGCAAGAAAGTACTTGTGACGAGAAAGAGCG 1285
Db      1295  GCATCGCTTCAATGTCTAGAGCGCTGCAAGAAAGTCTGTGACGAGAGGAGATG 1354
Oy      1286  GCGGCGCGCGCGA 1298
Db      1355  AGGAGGAGAGGA 1367

RESULT 7
US-10-425-114-25407
; Sequence 25407, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25407
; LENGTH: 1666
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3898-016-E4_FLI
US-10-425-114-25407

Query Match      41.4%; Score 672.8; DB 17; Length 1666;
Best Local Similarity 84.4%; Pred. No. 5.6e-173;
Matches 771; Conservative 0; Mismatches 133; Indels 9; Gaps 1;
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Db	817	GATTGGCCTCAACCTTGTGCACTTACCCCATGAGACTATCAAGCCAGGGTCACCATCG	876
Qy	815	AGAAAGACGTGTACGACAAACCTCTCCAAGCGTTTCGTCAAGATCTGTCGCGACGAAAGGCC	874
Db	877	AGAAAGACGTATACGACAAACGTGCGGACAGCGTTCTGTGAAGATCTTACGCCACGAGGCC	936
Qy	875	CGGGGAGACTGTATCCGCGGGCTGTGGCGCCGAGCTGATCGGCGGTGTGTCGTTACCGCGCGG	934
Db	937	CGTCGAGACTGTACCGTGGGCTGTACCCAGCTGTATCGGCGGTGTGTCGTTACCGCGGCT	996
Qy	935	CCAACTTTTAGCGCTTACGAGAGACGTGCGCGGCGGTATCCGCGCGCGCTTCGGGG-----	987
Db	997	GTAACTTTTAGCGCTTACGAGAGACGTGAGACGCGGCTTCACTGTCGCGCGACCGGGCGGCGCTC	1056
Qy	988	--AAAGAGAGGTGGGCAACGTCGCCGAGCGCTGTGATGGGGTCCGCGCGGGCCGCATAG	1045
Db	1057	CCGGCGCGAGACGTGGGGCCCCCGTGGGAGAGCTGTCTATGGGTCCGCGCGGGCCGCATCG	1116
Qy	1046	CCAGACAGGCAAGTTCCTCCGCTGTGAGAGTGGGCGCGGAAACAGTGCAGGTGGGCGCGCTGG	1105
Db	1117	CCAGTTCGAGCCAGTTCCTCCGCTGTGAGAGTGGGCGCGAAGAGTGCAGGTGGGCGCTGTGG	1176
Qy	1106	GGGGAGGCAAGTGTACAAAGAACGTGTCTGTGACGACCATGTACTGTCACTCTCGAAGAGAGG	1165
Db	1177	GGGGAGGCAAGTGTACCAAGAACGTCTCTCAAGCTATCTACTGTCACTCTTCAAGAAAGAGG	1236
Qy	1166	GCAACCGCGGAGCTTACCGCGGGGCTCGAGCCCCAGCTGTCAAGTCAAGTCAATGCCCCGCGG	1225
Db	1237	GCGCGGGCGGCTGTACCGAAGGTCTCGGCGCTTACGTGTCAAGTCAATGCCCCGCGCGG	1296
Qy	1226	GCAATTCCTTCAATGTGTCTACGAGGCGCTTGCAGAGAGATCTTGTGACGAGAAAGAGACG	1285
Db	1297	GCATGCGCTTCAATGTGTCTACGAGGCGGTCAAGAGATCTCTGTGACAAAGAGAGGATG	1356
Qy	1286	GCGGCGCGCGCGA	1298
Db	1357	AGGAGAGAGAGAGA	1369

Query Match	33.8%	Score 549;	DB 17;	Length 698;
Best Local Similarity	92.7%	Pred. No. 2.5e-139;		
Matches 600; Conservative	0;	Mismatches 40;	Indels 7;	Gaps 2;

476 ACTTTCGTCGGCTTGAGACCAATCAGACGCACCAGAATGGTAGGAGCTCCGCC 535

Db 594 CGCGGACGCCGTCACGTCGCCCGTTCGGCCACCAAGGCTTCGGCTTT 640

US-10-260-238-3968

Matches 619; Conservative 0; Mismatches 21; Indels 17; Gaps 5;

Db 347 CCAGGAGGACCGAGACCGACAGGACGAGGACGCGCGCCCAAGAGTCCACGG 406

QY 602 TCCGCGGCAACGCGTCAAGTCTCTCGCGCTCGCGCAAGCAAGGCCATCGAGCACTTCA 661
DB 941 TCCGTGGGAACCTTTGTAAATGTCATCCGAATGTCACCAAGCAAGGCTATTGAGCTATTG 1000
QY 662 CTTAACGACAGCGGCAAGAGTACTGAACCCCGAGGCGCGGAGCCAGCCAGGCTCCCA 721
DB 1001 CTTTTCATACAGCCAAAGAAATTTCTTAATCTCAAGAGGCTGATGAGTCCCTTAAGACCTT 1060
QY 722 TCCCGACGCGGCTGTGCGGAGCGCTCGCGGAGTGGGCTCAACCTGTGCACTATC 781
DB 1061 TCCCTCCATGCTTATGTCTGAGCACTGTGCGGTTAGCTCAACTTGCGACATTAAC 1120
QY 782 CCAATGAGCTGTCAAGACCGCTCTCAACATCGAAGAGAGCTGTACAGCAACCTCTCC 841
DB 1121 CTTGGAATGATTAAGAACCCGATTGACTATTGGAAGAGATGTCTTAATACAACTTCTCC 1180
QY 842 ACGGCTTCTCAAGATGCTGCGACGACAGAGCCCGGAGGAGCTGTACCGCGGCTGCGC 901
DB 1181 ATGCTTTGCTCAAGATTAATCAAGAGAGAGGCCCTCAAGACTTACCGCGGCTGACAC 1240
QY 902 CGAGCTGATGCGGCTGTGCTGCTGACGCGCGCACTTACGCTTACGAGACGCTGC 961
DB 1241 CGAGTCTGATGCGGCTGTGCTGCTGACGCGCACTTACGCTTACGAGACGCTGC 1300
QY 962 GCGGCGGTACCGCGCGGCTGCGGAGAGAGGAGTGGGCAAGTCCCGACGCTGTGA 1021
DB 1301 AGAAGCTTCAAGAGAGACATTTCAAGAGAGAGAGATCAAGACATGCGACTTCTCA 1360
QY 1022 TCGGCTCGCGGCGGCGGCTTACGACGAGCCAGCTTCCGCTGAGAGTGGCGGCA 1081
DB 1361 TCGGTTACGCGCGGCTGCTGCTGACGACCGGCACTTCCCTGAGAGTACCTGCA 1420
QY 1082 AGCAGATGAGGTGGCGCGTGGGCGGAGGCAAGGTGTAACAAGAGTGTGTCAGCCCA 1141
DB 1421 AGCAATGAGAGTGGGCGGCTGGGCGGAGGCAAGGTGTAACAAGAGTGTGTCAGCTC 1480
QY 1142 TGTCTGATCTCTGAGAGAGAGGCAACCGCGGCTTACCGGCGGCTGCGGCCAGCT 1201
DB 1481 TGTATTCATTAATGAGATTAAGAGATGAGGAGCTTTTACAGAGGCTTGGCGGAGCT 1540
QY 1202 GCATCAAGCTCATCCGCGCGGCACTTCTTCAATGCTACGAGGCTGCAAGAGA 1261
DB 1541 GCATCAAGCTCATCCGCGCGGCTGAGATCTCATTAATGCTTGAAGCTTGAAGAGA 1600
QY 1262 TACTTGTGACGAGAAAGAGACGCGC 1288
DB 1601 TACTGTTGAGATGATCAGGATAGTG 1627

RESULT 13
US-10-425-114-30842
Sequence 30842, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425.114
NUMBER OF SEQ ID NOS: 2003-04-28
SEQ ID NO 30842
LENGTH: 1516
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73089B03_FLI

US-10-425-114-30842
Query Match 29.4%; Score 477.2; DB 17; Length 1516;
Best Local Similarity 68.7%; Pred. No. 1.4e-119;
Matches 672; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
QY 311 CCGACGACGTTCGACACACAGCTCGACGCGGCGGAGCGGCGCTCCAGAGGCCAGA 370
DB 373 CTGAGGAGATGAGGATACAGGATTAATAGCACTGAACCGGAGTCACTGAGAGAGGTGG 432
QY 371 AGCGGAAAAAGGCCAAAAAGCAGCAGCTGATGTGAGGAAAGGAGGCAAGATCGGCA 430
DB 433 ATGCTAAGGCAAGAAAGGAGCCAAAGAAAGTGGGCTGACGCTGAATAATTAAATTTGG 492
QY 431 ACCGCACTGCGGCGGCTGATCAGCGGCGCATCCGCGGCGGCTGTGAGAGACTTTG 490
DB 493 ACCCAATTTGAGAGAGGCTGTATGAGAGCTATTGCAAGTGTGTTTCCAGGACTTGTG 552
QY 491 TGGCGCACTGAGAGAGATCAGACGACCTGATGTTGGGAGCTCCGCGCGGACTCCA 550
DB 553 TGGCACTGAGAGAGATCAGACGACCTGATGTTGGGAGCTCCGCGCGGACTCCA 609
QY 551 TGGCGGAGGTTTTCGCGGATCATGCGAGCGAGAGGAGGCGCGGCTTCCGCGGCA 610
DB 610 TGAAGAGGTTCAGTCAATCATGAACCTAAGAGGAGTGGAGCTTTCGTTGAGCA 669
QY 611 ACGCGGTCAAGCTCTCCGCTGCGCGCAAGCAAGGCACTGAGCACTTCACTTACGACA 670
DB 670 ATCTTGTCAATGTTATTCGAGTTGCGCGCAAGCAAGCAATTTGCTTTGATATA 729
QY 671 CCGGAGAAAGTACTGACCCCGAGAGCGCGGAGCCAGCAAGTCCCATCCCAAGC 730
DB 730 CTGCAAGAAATTTCTTGACTCAAGAGCTGATGATGCTTCAAGAGCTTCTCACTTCAT 789
QY 731 CGCTGCTGCGGAGGCTCCGCGAGTGGCGTCAACCTGTGCACTATCCATGAGAGC 790
DB 790 CACTTATGTGAGAGCACTTGAAGAGTCAAGCTTCAAGCTGTGCAATCTTGTGAGT 849
QY 791 TCGTCAAGACCGGCTTCAACCATGAGAGAGAGCTGTACGAACCTTCTTCAAGCTTGC 850
DB 850 TGATTAGACCAAGTTGACATAGAGAAAGATGTCTTAACAACTTCTCAAGCTTTCG 909
QY 851 TCAAGATCTGCGGAGAGAGCCCGGAGAGCTGTACCGGAGCTGGCGCGGAGCTGA 910
DB 910 TCAAGATTTTACGAGAAAGAGTCTCAAGAGCTTACCGTGTGTGACACCAAGTCTGA 969
QY 911 TCGCGTGTGCTGCTGAGCGCGGCACTTCAAGCTTACAGAGCTGCGGCGGT 970
DB 970 TAGGAGTGTGCAATAGCCGCACTAATTAATGACCTTAAGAGAGCTT 1029
QY 971 ACGCGCGGCTGCGGAGAGAGAGGTGGGCAAGTCCGAGCGCTGTATCGGCTCG 1030
DB 1030 ATTAGAGAGAGCTTACAGAGAGAGAGATCAGCAACATCGCACTCTCTAATTTGTTAG 1089
QY 1031 CCGCGGCGCATAGCAGAGCGGCACTTCCGCTGAGAGTGGCGCGGAGCAGATGC 1090
DB 1090 CCGCTGAGCATTCAGAGACCTGCACTTCCCTTTGAGAGTGGCGCGCAAGCAATATG 1149
QY 1091 AGGTGGCGCGTGGGAGGAGAGGTGTACAAAGACGTGTGCAAGCCATGTATCGCA 1150
DB 1150 AGGTAGGAGAGTATGAGAGAGAGGTGTACAAAGATGTGTTCAGTCCCTTATCGCA 1209
QY 1151 TCCGTGAGAGAGAGGAGCGCGGCTTACCGCGGCTGCGGCCAGCTGATCAAGC 1210
DB 1210 TAAATGAGAGAGAGGAGGTTGGCGGCTTACAGAGGAGCTTCCGACCGAGCTGATCAAGT 1269
QY 1211 TCAATGCGCGCGCGCATCTCTTCAATGTCTACAGAGGCTGTGCAAGATCTTGTG 1270
DB 1270 TGAATGCTGAGAGAGGATCTCTTCAATGTCTACAGAGGCTGTGAAAGATCTTGTG 1329
QY 1271 ACGAGAAAGAGACGCGC 1288
DB 1330 AAGCAATGAGAGATAGTG 1347

RESULT 14
 US-10-425-114-27699
 ; Sequence 27699, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaka, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21 (5313) B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 27699
 ; LENGTH: 1722
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB4738-065-E6_FLI
 US-10-425-114-27699

Query Match 29.4%; Score 477.2; DB 17; Length 1722;
 Best Local Similarity 68.7%; Pred. No. 1.4e-119;
 Matches 672; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
 311 CCGACGACGTGCGACACCACTCGACCGCGGGCGAGCGGCGCTCCAGAACGCCACA 370
 592 CTGAGGACGTTGGGTACAGCTTATTAACCTAAGCGAGTCACTGAGAGGAGTGTG 651
 371 AGCGCAAAAGGCCCAAAAGACAGCTGAGTCAAGAGTGAAGGCTCAAGATCGCA 430
 652 ATGCTAAGGCAGAAAGAGGAGCAAGCAAGTGGGGTGAAGTGAATTAATTAATGG 711
 431 ACCCGACCTCGCGCGCGCTGTGTCAGCGGCGCCATCGCGCGCGCTGTGAGGACTT 490
 712 ACCCAATTTGAGAGAGCTGTGTAGTGAAGTATTCAGGTGCTGTTTCCAGGACTT 771
 491 TGGCGCACTGAGAGATCAGACGCACTGATGTTGGGGGAGCTCCGCGCGGACTCCA 550
 772 TGGCACCACTGAGAGATCAGACTCACTTGAATGTTGAGCAACG--TGACTCCA 828
 551 TGGCCGCGGTTTCCGTTGATCATGCGAGCGAGGAGTGGCCGCTCTTCCGCGCA 610
 829 TGAAGAGGTGTTCAATCATATGAACATGAGGGGTGAGCTGGGCTTTCCGTGG 888
 611 AGCGCTCAACGCTCTCCGCGTGGCGCCCAAGCAAGCCATCGAGCACTTCACTTA 670
 889 ACTTGTCAATGTTATCCGAGTTGCGCAAGCAAAACAATGAGCTTTTGTGATA 948
 671 CGGCGAAGAGTACCTGACCCCGGAGCGCGGAGCGCAAGGATGCCATCCCAAGC 730
 949 CTGGCAAGAAATCTTGACTCCAAAGCTGATGATGCTCCAAAGACCTTCTACCT 1008
 731 CGCTCGCGCGAGCGCTCGCGAGTGGCGTCAACCTGTGCACTTCCATGGAGC 790
 1009 CACTTATGCTGAGAGCTTGAAGAGTCACTCAACCTGTGCAATATCTTTGAGT 1068
 791 TGTCAAGACCCGCTCAACCATGAGAGAGCTGTACGAACAACCTCTTCCAGCGT 850
 1069 TGAATTAAGACGATGAGATGAGAAAGATGTCTATAACAACCTCTTCAAGCTT 1128
 851 TCAAGATGAGCGAGAGCGCGAGCGCGGAGAGTGAACCGCGGCTGGGCGAGCTGA 910
 1129 TCAAGATTTTACAGAGAAAGGCTCATCAGAGCTTCAAGGTGTGAGAACCAAGCT 1188
 911 TGGCGCGGTTTCCGTTGATCATGCGAGCGGCACTTCAAGCTTCAAGAGCGCTG 970

Db 1189 TAGAGTGTGTCATATGCGCGACTAATTAATCAAGCTTATGACACCTTAAGAGCT 1248
 971 ACCGCGCGCGTCCGAGAAAGAGAGTGGGCAACGCTCCGAGAGCTGTATGGGTCG 1030
 1249 ATAGAAAGCTTCAAGCAGAGAGAGATCAGCAACATCGAACTCTCTAATGTTGAG 1308
 1031 CGGCGGCGCGCATAGCAGCAGCGGCAAGTCTCCGCTGAGAGTGGCGCGAGAGATGC 1090
 1309 CGCTGTGCTCATCTCAGAGACTGCACTTCCCTTGAAGTGGCGCGCAAGCAATGC 1368
 1091 AGGTGCGCGCGTGGCGAGGAGGAGGAGTGAAGAAAGTGTGACAGCGCATGTGCA 1150
 1369 AGGTAGAGAGAGTGAAGAGGAGGAGGAGGAGTGAAGAAAGTGTGACAGCGCT 1428
 1151 TCTCGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1210
 1429 TAATGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1488
 1211 TCATGCCCGCGCGCGCATCTCTTCAATGAGTGAAGAGGAGGAGGAGGAGGAGGAG 1270
 1489 TGAATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1548
 1271 ACGAGAAAGAGAGCGCG 1288
 1549 AAGACATGAGAGTAGTG 1566

RESULT 15
 US-10-425-115-13272
 ; Sequence 13272, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21 (5322) B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 13272
 ; LENGTH: 2090
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_112098C.1
 US-10-425-115-13272
 Query Match 29.4%; Score 477.2; DB 18; Length 2090;
 Best Local Similarity 68.7%; Pred. No. 1.5e-119;
 Matches 672; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
 311 CCGACGACGTGCGACACCACTCGACCGCGGGCGAGCGGCGCTCCAGAAAGGCCACA 370
 723 CTGAGGCAATTTGAGTACCGAGTTATTAAGCACTGAAGCGGAGTCAAGTGGTGG 782
 371 AGCGCAAAAGGCCCAAAAGAGCAGCTGAGTCTGAGAGGAGTGAAGGCTCAAGATCG 430
 783 ATGCTAAGGCAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 842
 431 ACCCGACCTGCGCGGCTGTGTCAGCGGCGCATGCGCGCGCGCTGTGAGAGACTT 490
 843 ACCCACTTTGAGAGGCTGTGTTAGTGAGCTATTGCAAGTGTCTGTTCAGAGACT 902
 491 TGGCGCACTGAGAGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 550
 903 TGGCACTGAGAGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 959
 551 TGGCGCGGTTTCCGTTGATCATGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 610
 960 TGAAGAGGTGTTCAATCATATGAACATGAGGGGTGAGCTGGGCTTTTCCGTGG 1019

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 06:27:14 ; Search time 423 Seconds
(without alignments)
6285.933 Million cell updates/sec

Title: US-10-659-199-17

Perfect score: 1625

Sequence: 1 ggcacagtcgagcgcgaagc.....aaaaaaaaaaaaaaaaa 1625

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
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6: /cgn2_6/prodata/1/ina/5B.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1625	100.0	1625	4 US-09-796-766-17	Sequence 17, Appl
2	400.2	24.6	1267	4 US-09-796-766-19	Sequence 19, Appl
3	392.6	24.2	449	4 US-09-796-766-15	Sequence 15, Appl
4	303	18.6	1089	4 US-09-796-766-13	Sequence 13, Appl
5	144	8.9	1062	4 US-09-796-766-3	Sequence 3, Appl
6	101.2	6.2	1816	4 US-09-188-930-262	Sequence 262, Appl
7	101.2	6.2	1816	4 US-09-312-283C-262	Sequence 262, Appl
8	94	5.8	986	4 US-09-270-767-1160	Sequence 1160, Appl
9	94	5.8	986	4 US-09-270-767-1160	Sequence 1160, Appl
10	89	5.5	1506	4 US-09-796-766-9	Sequence 9, Appl
11	89	5.5	1517	4 US-09-796-766-7	Sequence 7, Appl
12	79.6	4.9	504	4 US-09-796-766-11	Sequence 11, Appl
13	71.2	4.4	282	4 US-09-313-294A-1776	Sequence 1776, Appl
14	69.2	4.3	1779	4 US-09-902-540-3920	Sequence 3920, Appl
15	69.2	4.3	21375	4 US-09-902-540-1193	Sequence 1193, Appl
16	65	4.0	145	4 US-09-313-294A-1837	Sequence 1837, Appl
17	63	3.9	1431	4 US-09-724-797-87	Sequence 87, Appl
18	62.4	3.8	539	4 US-09-796-766-1	Sequence 1, Appl
19	61.2	3.8	6196	4 US-09-902-540-7880	Sequence 7880, Appl
20	61.2	3.8	1104	4 US-09-902-540-7880	Sequence 7880, Appl
21	61	3.8	237	4 US-08-987-367-5	Sequence 5, Appl
22	61	3.8	2742	4 US-09-252-991A-5556	Sequence 5556, Appl
23	61	3.8	3321	4 US-09-252-991A-5668	Sequence 5668, Appl
24	60	3.7	1689	4 US-09-252-991A-8717	Sequence 8717, Appl
25	60	3.7	1965	4 US-09-252-991A-9230	Sequence 9230, Appl
26	60	3.7	2805	4 US-09-252-991A-9064	Sequence 9064, Appl
27	59.4	3.7	1594	2 US-08-933-750C-61	Sequence 61, Appl

28	59.4	3.7	1594	3 US-09-234-613-61	Sequence 61, Appl
29	59.4	3.7	1594	4 US-09-976-594-710	Sequence 710, Appl
30	59.4	3.7	3889	4 US-09-902-540-492	Sequence 492, Appl
31	59.2	3.6	23673	3 US-09-773-816-1	Sequence 1, Appl
32	59	3.6	2028	4 US-09-902-540-7226	Sequence 7226, Appl
33	59	3.6	4377	4 US-09-902-540-676	Sequence 676, Appl
34	58.8	3.6	1350	4 US-09-902-540-918	Sequence 918, Appl
35	58.6	3.6	1350	4 US-09-799-451-799	Sequence 799, Appl
36	58.4	3.6	1566	4 US-09-620-312D-63	Sequence 63, Appl
37	58.4	3.6	1818	4 US-09-252-991A-2266	Sequence 2266, Appl
38	58.4	3.6	3051	4 US-09-252-991A-2343	Sequence 2343, Appl
39	58.4	3.6	3156	4 US-09-252-991A-2574	Sequence 2574, Appl
40	57.8	3.6	2658	4 US-09-252-991A-9558	Sequence 9558, Appl
41	57.8	3.6	2799	4 US-09-252-991A-9604	Sequence 9604, Appl
42	57.6	3.5	1288	1 US-08-440-856A-9	Sequence 9, Appl
43	57.6	3.5	3468	1 US-07-951-715A-2	Sequence 2, Appl
44	57.6	3.5	3468	2 US-08-459-448A-2	Sequence 2, Appl
45	57.6	3.5	3468	3 US-08-459-595A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-796-766-17

Sequence 17, Application US/09796766

Patent No. 6660850

GENERAL INFORMATION:

APPLICANT: Allen, Steve

APPLICANT: Lightner, Jonathan

APPLICANT: Rafalski, Antoni

TITLE OF INVENTION: BRITLYE-1 HOMOLOGS

FILE REFERENCE: BR1157 US CIP

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: US/09/796,766

PRIOR FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: 09/668884

PRIOR FILING DATE: 1999-03-22

PRIOR APPLICATION NUMBER: 60/079420

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Microsoft Office 97

SEQ ID NO 17

LENGTH: 1625

TYPE: DNA

ORGANISM: Triticum aestivum

US-09-796-766-17

Query Match 100.0%; Score 1625; DB 4; Length 1625;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCAGTGAAGGAGTGAAGAACTCTAGGCGAGGCGAGTATCACTTGTCT	60
DB	1	GGCAGTGAAGGAGTGAAGAACTCTAGGCGAGGCGAGTATCACTTGTCT	60
QY	61	TGCTTCTTGAGATGCGCGGCAATGCGGAGCAATGATGATCAAGAAACCGC	120
DB	61	TGCTTCTTGAGATGCGCGGCAATGCGGAGCAATGATGATCAAGAAACCGC	120
QY	121	GGCTGCTGCTGATGAGCAAGAAAGTATGCGGCGGCTCCCTAGTGGCTTC	180
DB	121	GGCTGCTGCTGATGAGCAAGAAAGTATGCGGCGGCTCCCTAGTGGCTTC	180
QY	181	CGTTGAGCTGCGACCGGAGTCCAGAGCTTGAATCCAGAGGAGCTGTTCGCC	240
DB	181	CGTTGAGCTGCGACCGGAGTCCAGAGCTTGAATCCAGAGGAGCTGTTCGCC	240
QY	241	AGCGTGAAGTCAAGCTTCCACCGCGCCCGCGATGCGCGAGCATGCGGAG	300
DB	241	AGCGTGAAGTCAAGCTTCCACCGCGCCCGCGATGCGCGAGCATGCGGAG	300

QY 301 GCTGCGCCCGCCGACGAGCTGCGACACCAAGCTCCGAGCCGCGGCGAGCGCGGCTCCAG 360
 Db 301 GCTGCGCCCGCCGACGAGCTGCGACACCAAGCTCCGAGCCGCGGCGAGCGCGGCTCCAG 360
 QY 361 AAGGCCAAGAAAGGAGAAAGGCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Db 361 AAGGCCAAGAAAGGAGAAAGGCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 AAGATCGGCAACCCGCGACCTGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCTG 480
 Db 421 AAGATCGGCAACCCGCGACCTGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCTG 480
 QY 481 AAGATCGGCAACCCGCGACCTGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCTG 540
 Db 481 AAGATCGGCAACCCGCGACCTGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCTG 540
 QY 541 GCGGACCTTCATGCGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 600
 Db 541 GCGGACCTTCATGCGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 600
 QY 601 TTCCGCGGCAACCCGCGACCTGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCTG 660
 Db 601 TTCCGCGGCAACCCGCGACCTGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCGGCTG 660
 QY 661 ACTTACGACACCGCGGAAAGAGTACCTGACCCCGGAGGCGCGGCGGCGGCGGCGGCGGCTG 720
 Db 661 ACTTACGACACCGCGGAAAGAGTACCTGACCCCGGAGGCGCGGCGGCGGCGGCGGCGGCTG 720
 QY 721 ATCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 780
 Db 721 ATCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 780
 QY 781 CCCATGAGAGCTGCGGAG 840
 Db 781 CCCATGAGAGCTGCGGAG 840
 QY 841 CAGCGGCTTCGCAAGAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 900
 Db 841 CAGCGGCTTCGCAAGAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 900
 QY 901 CCGAGGCTTCGCAAGAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 960
 Db 901 CCGAGGCTTCGCAAGAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 960
 QY 961 CCGAGGCTTCGCAAGAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1020
 Db 961 CCGAGGCTTCGCAAGAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1020
 QY 1021 ATCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1080
 Db 1021 ATCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1080
 QY 1081 AAGCAGATGCGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1140
 Db 1081 AAGCAGATGCGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1140
 QY 1141 AATGACGTCATCTTCGAGAAAG 1200
 Db 1141 AATGACGTCATCTTCGAGAAAG 1200
 QY 1201 TGCATCAAGCTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1260
 Db 1201 TGCATCAAGCTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1260
 QY 1261 ATACTTGTGCGAGAGAAAG 1320
 Db 1261 ATACTTGTGCGAGAGAAAG 1320
 QY 1321 GGAAGGCGAG 1380
 Db 1321 GGAAGGCGAG 1380
 QY 1381 TGAAGCATTTATGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1440

Db 1381 TGAAGCATTTATGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1440
 QY 1441 GTAGAGCTTATGCGAGTGAATCTTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 Db 1441 GTAGAGCTTATGCGAGTGAATCTTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 QY 1501 TTTGTTCAAGGAAAG 1560
 Db 1501 TTTGTTCAAGGAAAG 1560
 QY 1561 GTATCAATTCATTAAG 1620
 Db 1561 GTATCAATTCATTAAG 1620
 QY 1621 AAAA 1625
 Db 1621 AAAA 1625
 RESULT 2
 US-09-796-766-19
 ; Sequence 19, Application US/09796766
 ; Patent No. 660850
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Lightner, Jonathan
 ; APPLICANT: Rafalski, Antoni
 ; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
 ; FILE REFERENCE: BIL157 US CIP
 ; CURRENT APPLICATION NUMBER: US/09/796, 766
 ; PRIOR FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 09/668884
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/06583
 ; PRIOR FILING DATE: 1999-03-22
 ; PRIOR APPLICATION NUMBER: 60/079420
 ; PRIOR FILING DATE: 1998-03-26
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 19
 ; LENGTH: 1267
 ; TYPE: DNA
 ; ORGANISM: Trilicium aestivum
 US-09-796-766-19
 Query Match 24.6%; Score 400.2; DB 4; Length 1267;
 Best Local Similarity 66.8%; Pred. No. 1.2e-77;
 Matches 586; Conservative 0; Mismatches 288; Indels 3; Gaps 1;
 QY 415 AGGAGTCAAGTGGGCAACCGGACCTGCGGCGGCTGATCAGCGGCGGCGGCGGCGGCGGCTG 474
 Db 2 AAGATTAAAGGTGGAAATTCACCTCAAGAGGCTATCATGCGGCGGCGGCGGCGGCGGCTG 61
 QY 475 GTGTGAGAGCTTTCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 534
 Db 62 GTGTCAAGAGCAATTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 121
 QY 535 TCCGCGCGGAGCTTCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 594
 Db 122 AATGGGAATTCATCTACGAGAGGCTGTTGAC--TTCATCATGAAAGATGAAGATGAGACT 178
 QY 595 GGCCTCTTCGCGGCGGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 654
 Db 179 GGGTGTGTTCCGCGGCAATTTGGTTAATGTCATTCGATGCGGCGGCGGCGGCGGCGGCGGCGGCTG 238
 QY 655 CACTTCACTTACGACACGCGGAG 714
 Db 239 CTTTGTGCTTGTATACAGCTTAAG 298
 QY 715 GTCCCATCCCAACGCGGCTGCTGCGCGGAGCGGCTGCGGAGAGCGGCGGAGAGAGAGAGAGAGAG 774
 Db 299 ATCCCAATCCCTCTTCACTAGTGGCAGGAGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 358


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Db      67 GGGAGCTGTGGGCATAGTACATTCAGATGTTT---CAATCTATTATGAGACCGATGA 123
Qy      589 TGGCCCGGCTCTTCCCGGCAACGCCGTCAACGTCCTCCGCGTGGCCCAAGCAAGGCC 648
Db      124 TGGAAAGGCTTGTTCAGAGGCAATTTGTAAACATTCATCCAGATTGGCCCAAGCC 183
Qy      649 ATCGAGCACTTCACTTACGACACGCGAGAAAGTACTGACCCCGGAGCGCGGAGCCA 708
Db      184 ATTGAGTTATTGATATGACACTGTCAAGAAAGCAATTAATCTCCGAACCTCGAGAGCAG 243
Qy      709 GCCAAGTTCCTCAATCCCAAGCGCGCTGTGCGCCGAGAGCTCTCGCCGAGAGTGGCTCAAC 768
Db      244 CTTATTAATCCCAATTTCCCTCTCATCAATTCGGGATGTGTGTGTGTATGCTTAC 303
Qy      769 CTGAGCACTTATCCATAGAGCTGTCAAGACCGGTCACCATCGAAGAAAGATGTAC 828
Db      304 CTATGATCATACCTCTTGAATCTCAAACTGCGCTCACTGTTCAAGAGGGGTATC 363
Qy      829 GACAACCTCTCCACAGCGGTCGTCAAGATCTGCGGACGAAAGGCCGCGGAGACTGTAC 888
Db      364 AAGAACTTACTCGAAGCATTTGTGAGATGCTTCAAGAGAAAGTCTCGAGATTTGTAT 423
Qy      889 CGCGGCTGCGCGCGGAGCTGTATCGGCGTGTGCTGACGCGCGCAACTTCTACGCC 948
Db      424 AGGGGCTCGCGCTAGTCTAATGTGTATCCCTTATGCTGCAACAACTACTTGTCT 483
Qy      949 TAGAGAGCGTGGCGGGGCTGTACCGCGCGCTGGGGAAGAGAGTGGGCAAGTC 1008
Db      484 TATACACACTTAAAGAAAGCTTACAGAAAGCTTCAAAAGAGAGATTTGGAAATGTG 543
Qy      1009 CCGAGCGTGTGATCGGCTCCGCGCGGCGCCATAGCCACAGCAGCGCACGTTCCCGCTG 1068
Db      544 ATGACTCTTCTAATTTGATATGACGCTGTGTGCAATTTGAGTATGTGCAACTTCCACTT 603
Qy      1069 GAGGTGGCGGGAAGCAGATCAGGTGGGCGCGCTGGCGGAGGACAGTGTACAGAAAC 1128
Db      604 GAGGTGGCTGCTAAGCATATGCAAGCTGGGCTCTAAATGGAAGACA---ATATGGGAAC 660
Qy      1129 GTGCTGACGCGCATGTACTGTATCTGTGAGAAAGAGGAGCGACCGCGGGGCTTACCGGGG 1188
Db      661 ATGCTTATGACACTTGTGAGATATCTTGAAGAAAGAGAGTGTGTGCTGTATAGAGT 720
Qy      1189 CTCGCGCCCAAGCTCATCAAGCTCATGCCCCGCGCCGCACTCTTCATGTGCTACGAG 1248
Db      721 TTGGGACCAAGTCTTAAATTTGTTCTGTCTGTGGATTTCTTTCATGTGCTACGAA 780
Qy      1249 GCCTGCAAGAAATATCTTGTGACGAGAAAGAGA 1283
Db      781 GCTTGCAAGAGATATCTTGTGAAGAAATGAACAGA 815

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RESULT 5
US-09-796-766-3
; Sequence 3, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BRL157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1062

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; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-796-766-3
Query Match      8.9%; Score 144; DB 4; Length 1062;
Best Local Similarity 55.3%; Fred. No. 6.7e-22;
Matches 301; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

Qy      737 TCGCCGAGAGGCTCGCCGAGAGTGGCTCAACCTGTGCACTTATCCATAGAGCTGTGA 796
Db      204 TTCTGTGTGCGGCGCTGGAATTCGTGCACTTATGATGATCCATCTCTTGAAGTATTA 263
Qy      797 AGACCCGTCTACCATCGAAGAGAGTGTACGACCACTCTCCACGCGTGTCAAG 856
Db      264 AGATCGGCTGACCTGTGATTCGAGTGAATTCATCTTACATTTAGCATTTGCTCAGACA 323
Qy      857 TCGTGGCGACAGAGGCGCGGAGAGTGTACCGCGGCTGTGGCGCCGAGACTGTATGGGG 916
Db      324 TATATGAACTGAAGATATCAGAGTCTTATTTGAGCTTGTCCCAACACTAATTGGCA 383
Qy      917 TGGTGCCTTACGCGGCGGCACTTCTACGCTTACGAGACGCTGCGGCGTGTACCGCC 976
Db      384 TGCTTCTTACAGACATATGCTACTTATATGATCAATCAATCAAGAGTGTACTGCC 443
Qy      977 GCGCGTGGGGAAGAGAGTGGGCAAGTCCCAAGCTGTGATCGGATCGCGCGG 1036
Db      444 GCTTACATTAAGAAATCTTGTAGCGCTGTGAGCTTAAATTAAGAGCTGTACAG 503
Qy      1037 GCGCCATAGCAGACAGGCCAGTTCCGCTGAGAGTGTGCGGGAAGAGATGCAAGTGG 1096
Db      504 GTCTCAGGGAACAGATCAAGTCCGTTGGAGGTGCGAGGAAGCGGCTCATGATGG 563
Qy      1097 GCGCGTGGGCGGAGGAGCAAGTGTACAGAAAGTGTGACGCGCATGTGATCTCTG 1156
Db      564 GCGCCCTCAGAGGAGAGTGTGCGGCGGCAACA---TGTGCGCGGCTGTGAGAAATGATCC 620
Qy      1157 AGAAGAGAGGACCGCGCGGCTTACCGCGGCTGCGGCCCAAGTGCATCAAGCTATGC 1216
Db      621 GGGAGAGAGGCTCTCGGGGATCTACGTGGGTGGGCGAGCTCTCAAGGTATGC 680
Qy      1217 CCGCGCGCGCATCTCTTCAATGTGCTACGAGGCTGTCAAGAAAGATCTTGTGACAGAA 1276
Db      681 CGAATTCGGGCATCACTGATGTCTACGAGGCGTGAAGAGATATCTCTCGCGAGA 740
Qy      1277 AAGA 1280
Db      741 AAGA 744

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RESULT 6
US-09-188-930-262
; Sequence 262, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Iorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Omrusc, Rene
; APPLICANT: Muriison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-262
Query Match      6.2%; Score 101.2; DB 3; Length 1816;

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Best Local Similarity 48.6%; Pred. No. 1.6e-12;
Matches 413; Conservative 0; Mismatches 413; Indels 24; Gaps 4;

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QY 441 GGGGCGGCTGTGTCAGAGGCGCCATGCGCGGCGCGCTGTGAGGACTTTGTGGCGCCACT 500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 622 GAGGCACTGTGTGGCAGAGGTGGGCGAGGGGAGTTTCCAGAACTGCACTGCCCTT 681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 501 GAGAGCATCAGAGCAGCACTGTGTGGGAGCTCCGCGCGCCAGC-----TCCATGCG 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 682 GAGCAGACTGAAAGGTCTCATGTAGGCTCATGTCTCCCGACAGAACATGTGCTGT 741
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 555 CCGGGTTTTCCGGTGGATATGCGGACGAGGGGGTGGCCCGCTCTTCCGCGCAACGC 614
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 742 AGGTGATTCACACAGATGATTCAGAAAGGGGAGCAAGTCACTGCGGGGCAACGG 801
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 615 CGTCAACGTCTCCGCGTGGCGCCAGCAAGGCACTTCGAGCACTTCACTTACGACCGCG 674
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 802 CATCAATGTCTCAAAATTGCCCTGTAGTGGCCATCAAAATTCATGGCATATGACAGAT 861
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 675 GAAGAAGTACTGACCCCGGAGCGCGGAGCCAGCCAGCAAGTCCCATCCCAAGCGCGCT 734
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 862 GAAACGG-----CTTGTGGTATGTATCAGAGAGCGCTGAGGATCCAGAAAGCT 912
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 735 CGTCCCGGAGCGCTCGCGGAGTGGCTCAACCTGTGCACCTATCCCATGAGCTCGT 794
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 913 TGTGGCAGGCTCTTGGCCGAGCCATGTGCCAGAGTACATCTAACCAATGAGGTTCT 972
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 795 CAAGACCCGCTCAACATGAGAA---GGAAGTATACGACAACTCTCTCAAGCGCTTGT 851
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 973 GAAGACCCCAATGGCCCTCGGAGAAACAGAGACAGTATCTCCGACATGCTGACCTG 1032
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 852 CAAGATCGTGCAGAGGAGCCGAGGAGGAGCTGTACCGGGGCTGGGCGGAGCGCTGAT 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1033 GAGGATCTTGGCTAAAGAGGTGTAGCTCTTCTTCAAAAGCTTACATCCCAATGTCT 1092
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 912 CGGCGTGTGCGGTACGCGGCGGCAACTTCTACGCTTACGAGCGCTG-----CGCG 965
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1093 GGGGATTCATCCCTATGTGTGATGACCTAGCTGTATGAGACATTTGAAATAATCTG 1152
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 966 CGTGTACCGCGCGCGCTCGGGGAAAGAGAGGTGGCAAGTCCGACGCTGCTATCGG 1025
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1153 GCTTCAGGCGTACGAGTAAACAGTGCACACCCCGTGTCTGCTCTGCGCTGTGG 1212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1026 GTCCGCGGCGGCGCATATGACGAGCAGGCGAGTTCCTCCGCTGAGGTGGCGGAAAGA 1085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1213 TACTATCTTCACATCTTGTGGCAGCTGACCTACCACTAGCCCTGTGTCAAGACCG 1272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1086 GATGAGGTGGCGCGCTGGGCGGAGGAGGTGTACAGAAAGTGTCTCAAGCCATGTA 1145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1273 GATGAGGACAAAGCTCATATGAGGGGCGCACTGAGGTAAACATGAGAGCTCTTCA 1332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1146 CTGCACTCTCGAAGAGAGGCAACCGCGGCTCTTACCGCGGCTTGGCCCCAGCTGAT 1205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1333 ACAGATTTGTGCGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1206 CAAGCTCATGCGCGCGCGCGGATCTCTTCACTGTGTACGAGGCTGTGAATAAATCT 1265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1393 GAGGTGATCCCGCTGTGAGCATGACGTGTGTACGAAACCTGAAGATCACTCT 1452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1266 TGTGACGAG 1275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1453 GGGCGTGCAG 1462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 7
US-09-312-283C-262
; Sequence 262, Application US/09312283C

; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strichen, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene

; APPLICANT: Muriison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-262

Query Match 6.2%; Score 101.2; DB 4; Length 1816;
Best Local Similarity 48.6%; Pred. No. 1.6e-12;
Matches 413; Conservative 0; Mismatches 413; Indels 24; Gaps 4;

```

QY 441 GGGGCGGCTGTGTCAGAGGCGCCATGCGCGGCGCGCTGTGAGGACTTTGTGGCGCCACT 500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 622 GAGGCACTGTGTGGCAGAGGTGGGCGAGGGGAGTTTCCAGAACTGCACTGCCCTT 681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 501 GAGAGCATCAGAGCAGCACTGTATGTTGGGAGCTCCGCGCGCCAGC-----TCCATGCG 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 682 GAGCAGACTGAAAGGTCTCATGTAGGCTCATGTCTCCCGACAGAACATGTGCTGT 741
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 555 CCGGGTTTTCCGGTGGATATGCGGACGAGGGGTGGCCCGGCTCTTCCGCGCAACGC 614
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 742 AGGTGATTCACACAGATGATTCAGAAAGGGGAGCAAGTCACTTGGCGGGGCAACGG 801
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 615 CGTCAACGTCTCCGCGTGGCGCCAGCAAGGCACTTCAGCACTTCACTTACGACCGCG 674
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 802 CATCAATGTCTCAAAATTGCCCTGTAGTGGCCATCAAAATTCATGGCATATGACAGAT 861
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 675 GAAGAAGTACTGACCCCGGAGCGCGGAGCCAGCCAGAGTCCCATCCCAAGCGCGCT 734
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 862 GAAACGG-----CTTGTGGTATGTATCAGAGAGCGCTGAGGATCCAGAAAGCT 912
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 735 CGTCCCGGAGCGCTCGCGGAGTGGCTCAACCTGTGCACCTATCCCATGAGCTCGT 794
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 913 TGTGGCAGGCTCTTGGCCGAGCCATGTGCCAGAGTACATCTAACCAATGAGGTTCT 972
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 795 CAAGACCCGCTCAACATGAGAA---GGAAGTATACGACAACTCTCTCAAGCGCTTGT 851
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 973 GAAGACCCCAATGGCCCTCGGAGAAACAGAGACAGTATCTCCGACATGCTGACCTG 1032
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 852 CAAGATCGTGCAGAGGAGCCGAGGAGGAGCTGTACCGGGGCTGGGCGGAGCGCTGAT 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1033 GAGGATCTTGGCTAAAGAGGTGTAGCTCTTCTTCAAAAGCTTACATCCCAATGTCT 1092
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 912 CGGCGTGTGCGGTACGCGGCGGCAACTTCTACGCTTACGAGCGCTG-----CGCG 965
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1093 GGGGATTCATCCCTATGTGTGATGACCTAGCTGTATGAGACATTTGAAATAATCTG 1152
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 966 CGTGTACCGCGCGCGCTCGGGGAAAGAGAGGTGGCAAGTCCGACGCTGCTATCGG 1025
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1153 GCTTCAGGCGTACGAGTAAACAGTGCACACCCCGTGTCTGCTCTGCGCTGTGG 1212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1026 GTCCGCGGCGGCGCATATGACGAGCAGGCGAGTTCCTCCGCTGAGGTGGCGGAAAGA 1085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1213 TACTATCTTCACATCTTGTGGCAGCTGACCTACCACTAGCCCTGTGTCAAGACCG 1272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1086 GATGAGGTGGCGCGCTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1273 GATGAGGACAAAGCTCATATGAGGGGCGCACTGAGGTAAACATGAGAGCTCTTCA 1332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1146 CTGCACTCTCGAAGAGAGGCAACCGCGGCTCTTACCGCGGCTTGGCCCCAGCTGAT 1205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1333 ACAGATTTGTGCGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1206 CAAGCTCATGCGCGCGCGGATCTCTTCACTGTGTACGAGGCTGTGAATAAATCT 1265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 1393 GAAGTGATCCCGCTGTGACATCAAGTACTGTCTACGAAACCTGAAATCACTT 1452
QY 1266 TGTGACGAG 1275
Db 1453 GGGCGTGAG 1462

RESULT 8

US-09-270-767-1160
; Sequence 1160, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1160
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1160

Query Match 5.8%; Score 94; DB 4; Length 986;

Best Local Similarity 49.8%; Pred. No. 5e-11;
Matches 303; Conservative 0; Mismatches 290; Indels 15; Gaps 2;

QY 673 GCGAAGAGTACTGACCCCGAGCCGCGAGCCAGCCAGATCCCATCCCGACCG 732
Db 40 GAGACAGTGGGTGTCATCTGTGACATGACGACGAGGACGACCAACAGAAAGTGTGCG 99
QY 733 CTGCTGCCGAGCGCTGCGCGAGTGGCGTCAACCTGTGCACTTATCCCATGAGACTC 792
Db 100 TTTTGGCTGGCTCCCTGCGGGAATCACTCAAGTGTGAGTATCTCTGAGACTG 159
QY 793 GTCAAGACCCGTCTCAACATC-----GAGAAGACGTGTACGACAACTCTCCAGCG 846
Db 160 GCACGCGCCCGCATGCGCGGTACGAGATCGGTATCTGCTATCGAGCGTGTGCAAGTC 219
QY 847 TTCGTCAAGATCTGTGCGCGAGAGAGCCCGGAGCTGTACCGCGGCTGGCGCGAGC 906
Db 220 TTTCACCAAGATCTGTGAGAGAGGTTCGCGAGCGCTTCCGCGGTACTGGGCAAC 279
QY 907 CTGATCGCGGTGTGCTGCGGTACGCGCGCACTTCTACGCTTACGAGCGCTGCGCGC 966
Db 280 GTTCTCGGCGTGTATCCCTATGCGGGCACTCTTCTTCACTACGAGACTCTTAAGCG 339
QY 967 GTGTACCGCGCGGTGGGGGAAAGAGAGGTGGGCAACGTCGAGCGTGTGAGG 1026
Db 340 GAATATCTATGATGTGTGCGGCAATTAACCCAAATCTTATGTTCTACCTGCGCTTGGT 399
QY 1027 TCCGCGCGCGCGCATAGCCAGCAGCCAGCTTCCCGCTGAGTGGCGCG----- 1079
Db 400 GCTGCGGCTGTGCGCGCGGCAACGCGGCAATCATTTGGAATTGTGGCGGAG 459
QY 1080 --GAAGACATGAGTGGGCGCGGTGGGCGGAGCGAGTGTACAAAGAGTGTGAC 1137
Db 460 ATGACAGCAATGCGGGTGAACACGCGTGGCGAGATCGTACCCAACTCTTGAAGCT 519
QY 1138 GCCATGTATGTCATCTCGAAGAGAGAGGCGCGCGGCTTACCGGCGGCTGGCGCC 1197
Db 520 CTGTCAAGATCTATCTGTGAGAGGCGGTCAAGAGGTTTCTACAGAGGCTTAAGATG 579
QY 1198 AGCTGATCAAGCTCATGCGCGCGCGGCTATCTCTTCAATGATGTCTACGAGGCTGCA 1257
Db 580 AACTGATCAAGAGGAGCCATGCGCGGTGGGCTATCAAGCTTCTCACTACGATCTGATCAG 639
QY 1258 AAGATCT 1265
Db 640 GCGTGGCT 647

RESULT 9

US-09-270-767-16442
; Sequence 16442, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16442
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16442

Query Match 5.8%; Score 94; DB 4; Length 986;

Best Local Similarity 49.8%; Pred. No. 5e-11;
Matches 303; Conservative 0; Mismatches 290; Indels 15; Gaps 2;

QY 673 GCGAAGAGTACTGACCCCGAGCCGCGAGCCAGCCAGATCCCATCCCGACCG 732
Db 40 GAGACAGTGGGTGTCATCTGTGACATGACGAGGAGGACGACCAACAGAAAGTGTGCG 99
QY 733 CTGCTGCCGAGCGCTGCGCGAGTGGCGTCAACCTGTGCACTTATCCCATGAGACTC 792
Db 100 TTTTGGCTGGCTCCCTGCGGGAATCACTCAAGTGTGAGTATCTCTGAGACTG 159
QY 793 GTCAAGACCCGTCTCAACATC-----GAGAAGACGTGTACGACAACTCTCCAGCG 846
Db 160 GCACGCGCCCGCATGCGCGGTACGAGATCGGTATCTGCTATCGAGCGTGTGCAAGTC 219
QY 847 TTCGTCAAGATCTGTGCGCGAGAGAGCCCGGAGCTGTACCGCGGCTGGCGCGAGC 906
Db 220 TTTCACCAAGATCTGTGAGAGAGGTTCGCGAGCGCTTCCGCGGTACTGGGCAAC 279
QY 907 CTGATCGCGGTGTGCTGCGGTACGCGCGCACTTCTACGCTTACGAGCGCTGCGCGC 966
Db 280 GTTCTCGGCGTGTATCCCTATGCGGGCACTCTTCTTCACTACGAGACTCTTAAGCG 339
QY 967 GTGTACCGCGCGGTGGGGGAAAGAGAGGTGGGCAACGTCGAGCGTGTGAGG 1026
Db 340 GAATATCTATGATGTGTGCGGCAATTAACCCAAATCTTATGTTCTACCTGCGCTTGGT 399
QY 1027 TCCGCGCGCGCGCATAGCCAGCAGCCAGCTTCCCGCTGAGTGGCGCG----- 1079
Db 400 GCTGCGGCTGTGCGCGCGGCAACGCGGCAATCATTTGGAATTGTGGCGGAG 459
QY 1080 --GAAGACATGAGTGGGCGCGGTGGGCGGAGCGAGTGTACAAAGAGTGTGAC 1137
Db 460 ATGACAGCAATGCGGGTGAACACGCGTGGCGAGATCGTACCCAACTCTTGAAGCT 519
QY 1138 GCCATGTATGTCATCTCGAAGAGAGGCGCGCGGCTTACCGGCGGCTGGCGCC 1197
Db 520 CTGTCAAGATCTATCTGTGAGAGGCGGTCAAGAGGTTTCTACAGAGGCTTAAGATG 579
QY 1198 AGCTGATCAAGCTCATGCGCGCGCGGCTATCTCTTCAATGATGTCTACGAGGCTGCA 1257
Db 580 AACTGATCAAGAGGAGCCATGCGCGGTGGGCTATCAAGCTTCTCACTACGATCTGATCAG 639
QY 1258 AAGATCT 1265
Db 640 GCGTGGCT 647

RESULT 10

US-09-796-766-9
; Sequence 9, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:

```

; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-796-766-9

```

```

Query Match      5.5%; Score 89; DB 4; Length 1506;
Best Local Similarity 49.0%; Pred. No. 7e-10;
Matches 267; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

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```

QY 735 CGTCCGCGGAGCGCTGCGCGGAGTGGCTCAACCCCTGTGACCTATCCCATGAGAGCTCGT 794
DB 702 CATCCGCGGTGACGCTGCTGGAATGCTAGCACTCTTGATGCACTCCCTTGAACTTTT 761
QY 795 CAAGACCCGCTCTACCATCGAGAAGACGTGTACGAAACCTCTCCACGCTTCTCTCA 854
DB 762 GAAAGACCGGTTTAACTGTAAGTCTGAAACTTAACCTTAAGCATTTGAGCATTTGAAA 821
QY 855 GATCGTGGCGGAGAGAGCGCCGCGGAGCTGTACCGCGGCTGGCGCCGAGCCTGATCGG 914
DB 822 TATTTAATAAAGACGAGGAGTGTGGCGCTTTTATGCTGATCTCAACAACCTGGTTGG 881
QY 915 CGTGGGCGGCTACCGCGCGGCGCAACTTCAACGCTTACGAGACGCTGGCGGCGGTGACCG 974
DB 882 CATTGCTTCATACAGTACATGTTTTTATTTCATGTAATGATACAAATTAAGAACTTACG 941
QY 975 CCGCGCGTGGGAGAAAGAGAGGTGGCAACGTCGCCGACGCTGCTGATCGGCTCGCGCG 1034
DB 942 CCGGACCAAAAGTAAGAAATCTCTAAGCCGTCCAGAGATGCTTTGATTTGAGCTTTC 1001
QY 1035 GGGCGCCATAGCCAGACGCGCAAGTTCCTCGCTGAGGTGGCGCGGAGCAGATGCAAGT 1094
DB 1002 AGGTTTACTGCAAGTACATTAAGCTTCCCTTGAGGTAGCAAGAGACGCTGATGGT 1061
QY 1095 GGGCGCCGCGGAGGAGGAGGAGGTGTACAAAGACGTGTGACAGCCATGTACTGATCCT 1154
DB 1062 GGGTCTTTGCAAGGTAAAGTGGCCG--CCAAACATGGGAGCGGCACTTTCAGAAATTAT 1118
QY 1155 CGAGAAGAGGAGGACCGCGGCTCTACCGCGGAGCTCGGCCACAGCTGATCAAGCTCAT 1214
DB 1119 TAGAAGAAAGGTCTGAAGGCTCTTACAGAGAGATGGGCTGAAGCTGTTTAAAGTCA 1178
QY 1215 GCCCGCGCGGAGCTCTCTTATGTGTACAGAGGCTGCAAGAAATATTGTGACAGA 1274
DB 1179 GCCATCTCTGTATACACTGATGTTTATGAAAGCTTGAAAGACATATTGCTGTCCA 1238
QY 1275 GAAAG 1279
DB 1239 GAATG 1243

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RESULT 11
US-09-796-766-7
; Sequence 7, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan

```

```

; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1517
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-796-766-7

```

```

Query Match      5.5%; Score 89; DB 4; Length 1517;
Best Local Similarity 49.0%; Pred. No. 7e-10;
Matches 267; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

```

```

QY 735 CGTCCGCGGAGCGCTGCGCGGAGTGGCTCAACCCCTGTGACCTATCCCATGAGAGCTCGT 794
DB 697 CATCCGCGGTGACGCTGCTGGAATGCTAGCACTCTTGATGCACTCCCTTGAACTTTT 756
QY 795 CAAGACCCGCTCTACCATCGAGAAGACGTGTACGAAACCTCTCCACGCTTCTCTCA 854
DB 757 GAAAGACCGGTTTAACTGTAAGTCTGAAACTTAACCTTAAGCATTTGAGCATTTGAAA 816
QY 855 GATCGTGGCGGAGAGAGCGCCGCGGAGCTGTACCGCGGCTGGCGCCGAGCCTGATCGG 914
DB 817 TATTTAATAAAGACGAGGAGTGTGGCGCTTTTATGCTGATCTCAACAACCTGGTTGG 876
QY 915 CGTGGGCGGCTACCGCGCGGCGCAACTTCAACGCTTACGAGACGCTGGCGGCGGTGACCG 974
DB 877 CATTGCTTCATACAGTACATGTTTTTATTTCATGTAATGATACAAATTAAGAACTTACG 936
QY 975 CCGCGCGTGGGAGAAAGAGAGGTGGCAACGTCGCCGACGCTGCTGATCGGCTCGCGCG 1034
DB 937 CCGGACCAAAAGTAAGAAATCTCTAAGCCGTCCAGAGATGCTTTGATTTGAGCTTTC 996
QY 1035 GGGCGCCATAGCCAGACGCGCAAGTTCCTCGCTGAGGTGGCGCGGAGCAGATGCAAGT 1094
DB 997 AGGTTTACTGCAAGTACATTAAGCTTCCCTTGAGGTAGCAAGAGACGCTGATGGT 1056
QY 1095 GGGCGCCGCGGAGGAGGAGGAGGTGTACAAAGACGTGTGACAGCCATGTACTGATCCT 1154
DB 1057 GGGTCTTTGCAAGGTAAAGTGGCCG--CCAAACATGGGAGCGGCACTTTCAGAAATTAT 1113
QY 1155 CGAGAAGAGGAGGACCGCGGCTCTACCGCGGAGCTCGGCCACAGCTGATCAAGCTCAT 1214
DB 1114 TAGAAGAAAGGTCTGAAGGCTCTTACAGAGAGATGGGCTGAAGCTGTTTAAAGTCA 1173
QY 1215 GCCCGCGCGGAGCTCTCTTATGTGTGTACAGAGGCTGCAAGAAATATTGTGACAGA 1274
DB 1174 GCCATCTCTGTATACACTGATGTTTATGAAAGCTTGAAAGACATATTGCTGTCCA 1233
QY 1275 GAAAG 1279
DB 1234 GAATG 1238

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```

RESULT 12
US-09-796-766-11
; Sequence 11, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS

```


QY 1047 CACACGCGCCACGCTTCCCGCTGAGGTGCGCGAGACAGATGAGGTGGCCCGCTGGG 1106
 DB 885 CGCGGTGTCCACGCTGCGCACCGGGTTCCGGAGAGAGGTGTATCCGATCTTTCCAGCC 944
 QY 1107 CGGAGAGCAGGTGTACAGAACTGCTGTCACGCCATGTACTGATCTCTGAGAGAGAGG 1166
 DB 945 GAGAGAGCTGTGTACAGAGACATCCCGGCTTCCAGCTTCCAGCCAGAGAGAGAGCGCTT 1004
 QY 1167 CACGCGCGGCTTACCGCGGGGCTCCGCGCCAGCTGATCAACTCATGCGCCCGCGCGG 1226
 DB 1005 CGAGTCTGTGATTTACACGACACAGGCTTATCTGTACAGGCGCCCAACGAGCGG 1064
 QY 1227 CATCTCTTCAATGTGTACAGAGCTTGCAGAGATTAATTGTGACAGAGAAAGAGCGG 1286
 DB 1065 GAAAGAGAGAGAGCGCTTACTCCGCTCAAGGGGCTGCGCGCGCCGAGCTCAAGCTCAC 1124
 QY 1287 CGGCGCGCGCGAGCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1346
 DB 1125 CACCATCGAAGAGCCCATCGAATGAGTGTGGACGCTTCAACAGGTGAGGTGACGCC 1184
 QY 1347 CAAG 1350
 DB 1185 CAAG 1188

RESULT 15

US-09-902-540-1193
 / Sequence 1193, Application US/09902540
 / Patent No. 6833447
 / GENERAL INFORMATION:
 / APPLICANT: Goldman, Barry S.
 / APPLICANT: Hinkle, Gregory J.
 / APPLICANT: Slater, Steven C.
 / APPLICANT: Wiegand, Roger C.
 / TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 / FILE REFERENCE: 38-10(15849)B
 / CURRENT APPLICATION NUMBER: US/09/902,540
 / PRIOR FILING DATE: 2001-07-10
 / PRIOR APPLICATION NUMBER: 60/217,883
 / NUMBER OF SEQ ID NOS: 16825
 / SEQ ID NO 1193
 / LENGTH: 21375
 / TYPE: DNA
 / ORGANISM: Myxococcus xanthus
 / FEATURE:
 / NAME/KEY: unsure
 / LOCATION: (1)..(21375)
 / OTHER INFORMATION: unsure at all n locations
 US-09-902-540-1193

Query Match 4.3%; Score 69.2; DB 4; Length 21375;
 Best Local Similarity 43.1%; Pred. No. 3.3e-05;
 Matches 390; Conservative 0; Mismatches 508; Indels 6; Gaps 1;

QY 447 GGTGTACAGCGCGGCTTACGCGGCGCGGCTTGTGAGAGACTTGTGCGGCACTGAGAC 506
 DB 19767 GCTGGCAGCGCGACGCTGTCCAGGCTTACCGGAGAGACAGCTGTCTTCCCTGGA 19826
 QY 507 GATCAGAGACGCACTGATGATGGAGAGCTCCGCGCGGCACTCCATGAGCGGGGTTTCCG 566
 DB 19827 GCGCAGCGCGCGCGGCTGTGTGTGGGCGGCAACCTTTGACCGGGAACCTTT 19886
 QY 567 GTGATCATGCGGAGAGAGAGGCTGCGCGGCTTTCGCGGCGCAAGCGTCAAGCTCT 626
 DB 19887 CGAAGACTTCAACGCGCTGACGGGGCTGCGGAGAGCCGCTCAGCGCGAAGCGGA 19946
 QY 627 CGCGCTGCGCGCAAG 686
 DB 19947 CATCTCAAGTCTCATAGGAGACTTACGAGCTTCAAGAGAGAGAGAGAGAGAGAG 20006
 QY 687 GACCCCGAGCGCGGAG 746

DB 20007 CGACTTCAGGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20066
 QY 747 GCTTGGCGAG 806
 DB 20067 CGGCACTCAG 20126
 QY 807 CACCATCGAAG 866
 DB 20127 GCGCTTACGAG 20186
 QY 867 CGAAGCGCGGAG 926
 DB 20187 CGTGTGCGCTTCCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20246
 QY 927 CGGCGCGCGCACTTTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 986
 DB 20247 GCATCCGCGCATCTGTCTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20306
 QY 987 GAAAG 1046
 DB 20307 CAGCGCGAG 20360
 QY 1047 CAGCAGCGCCAGCTTCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1106
 DB 20361 CGCGGTGTCCAGCTGCGCACCGCGCTTCCGCGAGAGAGAGAGAGAGAGAGAGAGAG 20420
 QY 1107 CGGAG 1166
 DB 20421 GAG 20480
 QY 1167 CACCGCGGAGCTTACCGGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1226
 DB 20481 CGAGTCTGATTTACAG 20540
 QY 1227 CATCTCTTCAATGTGTACAG 1286
 DB 20541 GAAAG 20600
 QY 1287 CGGCGCGCGAG 1346
 DB 20601 CACCATCGAAG 20660
 QY 1347 CAAG 1350
 DB 20661 CAAG 20664

Search completed: May 25, 2005, 12:31:49
 Job time : 426 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 06:24:34 ; Search time 8067 Seconds
(without alignments)
7667.588 Million cell updates/sec

Title: US-10-659-199-17

Perfect score: 1625

Sequence: 1 ggcacgtggggagtgaggg.....aaaaaaaaaaaaaaaaaaaaa 1625

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: gb_esc1:*
2: gb_esc2:*
3: gb_hnc:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	689.4	42.4	722	6	CD885431 G118.001H
2	680.8	41.9	722	5	BQ807247 WHE358.E
3	663.6	40.8	856	5	AM448477 BRY_866.B
4	663.6	40.8	856	5	BQ609855 BRY_866.W
5	645	39.7	655	5	BQ606434 BRY_2295
6	640.6	39.4	710	7	CV054670 BNE11244
7	639.6	39.4	787	2	AM448382 BRY_646.B
8	639.6	39.4	787	2	BQ609766 BRY_646.W
9	594.4	36.6	686	5	BQ608893 BRY_4808
10	593.4	36.6	700	1	AL506887 AL506887
11	592.2	36.4	700	1	AL507153 AL507153
12	577.8	35.6	700	1	AL506597 AL506597
13	573.6	35.3	897	6	CD433626 EL01N0313
14	559.2	34.4	784	2	BE413774 SCU002.H0
15	555.6	34.2	739	7	CK125192 BES182410
16	552	34.0	611	1	AL814614 AL814614
17	550.6	33.9	591	5	BQ241079 TAB05009D
18	549	33.8	550	5	BQ606767 BRY_2638
19	548.2	33.7	737	7	CK122138 BES182410
20	546.8	33.6	589	5	BQ609479 BRY_5410
21	540	33.2	765	6	CD434709 EL01N0327
22	538.8	33.2	559	4	BJ235011 BJ235011
23	535.6	33.0	577	5	BQ240466 TAB05017A
24	535.6	33.0	578	5	BQ606681 BRY_2549

25	532.6	32.8	588	5	BQ804590
26	532.4	32.8	593	1	AL810557
27	529.2	32.6	622	7	CV055671 WHE125B8
28	528	32.5	669	2	BE414349 SCU008.G0
29	526.2	32.4	576	5	BQ239046 TAB05037H
30	522.2	32.1	607	5	BQ238019 TAB05009D
31	522	32.1	539	5	BQ608979 BRY_4897
32	520	32.0	574	2	BE402432 CSB007H06
33	520	32.0	574	5	BQ607768 BRY_3663
34	512.4	31.5	524	2	AM448856 BRY_1667
35	512.4	31.5	524	5	BQ606051 BRY_1667
36	510.8	31.4	751	6	CD438567 EL01N0514
37	509.2	31.3	539	2	BE402546 CSB009A12
38	509.2	31.3	539	5	BQ608240 BRY_4128
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40	505.4	31.1	553	7	CV058864 BNE141H1
41	502.8	30.9	548	1	AL812274 AL812274
42	496.2	30.5	548	5	BQ240186 TAB05021A
43	492.4	30.3	754	6	CD448019 EL01N0203
44	488.2	30.0	517	5	BQ606900 BRY_2776
45	482	29.7	482	2	BE402735 CSB011A09

ALIGNMENTS

RESULT 1
CD885431 724 bp mRNA linear EST 14-JUL-2003
LOCUS G118.001H02F010306 G118 Triticum aestivum cDNA clone G118001H02,
DEFINITION mRNA sequence.

ACCESSION CD885431 GI:32650608
VERSION CD885431.1
KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
1 (bases 1 to 724)

AUTHORS Genoplatte.
TITLE Genoplatte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplatte

Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source
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/organism="Triticum aestivum"
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/db_xref="taxon:4565"
/clone="G118001H02"
/issue_type="grain (118 degree per day after
pollination)"
/clone_11b="G118"

ORIGIN

Query Match 42.4%; Score 689.4; DB 6; Length 724;
Best Local Similarity 97.0%; Pred. No. 9e-144;
Matches 702; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 14 GTGAAGACTGAAAGACTCTTGAAGGACGATCTGCTTGTCTTCTTCGAGA 73
DB 1 GTGAAGACTGAAAGACTCTTGAAGGACGATCTGCTTGTCTTCTTCGAGA 60
QY 74 TGGCGCGCATATGCGCGGACGACGACATGTGACCAAGAACACCGCGCTCGTCGA 133

Db 61 TGGCGCGGCAATGCGGCAACGACATGATGACCAAGAACACCGGCTCGCTGCCA 120
 QY 134 TGGACAAGAGAACTGGATTATTCGGCCCGCTGAGTCCCTTGCCTTGGAGCTCGC 193
 Db 121 TGGACAAGAGAACTGGATTATTCGGCCCGCTGAGTCCCTTGCCTTGGAGCTCGA 180
 QY 194 AGCCCGAGTCCAGAGCTTGGATCTTCCACAGCAGGCTCTGTTCCGACAGCTGGAGCTCA 253
 Db 181 AGCCCGAGTCCAGAGCTTGGATCTTCCACAGCAGTGGCTCTGTTCCGACAGCTGGAGCTCA 240
 QY 254 GCTGTGCCAAGCGCGCCCGCGGTAGCGCGCAGCATGACGGGAAAGCTCGCCCGCG 313
 Db 241 GCTGTGCCAAGCGCGCCCGCGGTAGCGCGCAGCATGACGGGAAAGCTCGCCCGCG 300
 QY 314 AGCAGCTGCAACACAGCTGCAAGCCGCGGCGAGCGCGGCTTCAGAGCCCAAGG 373
 Db 301 AGCAGCTGCGACACAGCTGCAAGCCGCGGCGAGCGCGGCTTCAGAGCCCAAGG 360
 QY 374 GAAAAAGGCAAAAAAGCAGCAGCTGATGCTGAGGAAAGTGAAGTCAAGATCGGCAAC 433
 Db 361 GAAAAAGGCAAAAAAGCAGCAGCTGATGCTGAGGAAAGTGAAGTCAAGATCGGCAAC 420
 QY 434 GGAACCTGCGGCGGCTGTCAGCGCGCGCAATCGCGCGCGCTGTCAGAGACTTTCGTG 493
 Db 421 GGAACCTGCGGCGGCTGTCAGCGCGCGCAATCGCGCGCGCTGTCAGAGACTTTCGTG 480
 QY 494 CGCCACTGAGACAGATCAGACGCGACCTGATGCTGAGGAGCTCGCGCGCGACTCCATG 553
 Db 481 CGCCCTGAGAGAGATCAGAGCGCGACCTGATGCTGAGGAGCTCGCGCGCGACTCCATG 540
 QY 554 CGGCGGCTTTTCGCTGATATGCGGACAGAGGCGTGGCCCGGCTTCCGCGGCAAG 613
 Db 541 CGGCGGCTTTTCGCTGATATGCGGACAGAGGCGTGGCCCGGCTTCCGCGGCAAG 600
 QY 614 CGGTCAGCTCTCGCGGTGCGCGCAAGCAAGGCGCATTCAGAGCTTCAGACAGCG 673
 Db 601 CGGTCAGCTCTCGCGGTGCGCGCAAGCAAGGCGCATTCAGAGCTTCAGACAGCG 660
 QY 674 CGAAGAGTACTCTGATCCCGGAGCGCGGAGCGAGCCAGGTCCTCCATCCCAAGCGCGC 733
 Db 661 CGAAGAGTACTCTGATCCCGGAGCGCGGAGCGAGCCAGGTCCTCCATCCCAAGCGCGC 720
 QY 734 TCGT 737
 Db 721 TCGT 724

RESULT 2
 B0807247 722 bp mRNA linear EST 31-JUL-2002
 LOCUS WHB3588 E08.11625 wheat developing grains cDNA library Triticum
 DEFINITION aestivum cDNA WHB3588_E08.116, mRNA sequence.
 ACCESSION B0807247
 VERSION B0807247.1 GI:22031456
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.
 1 (bases 1 to 722)
 Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J.,
 Cronin,K., Crossman,C., Fenton,R.D., Iazo,G.R., Pham,J.,
 Rausch,C.J., Wilson,C. and Woo,J.
 The structure and function of the expressed portion of the wheat
 genomes - Developing grains cDNA library
 Unpublished (2002)
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105959773
 Fax: 5105959818

FEATURES
 source
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 /organism="Triticum aestivum"
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 /cuiovar="Putte 86"
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 /clone_lib="wheat developing grains cDNA library"
 /note="Vector: Lambda ZAP II, excised phagemid; Site 1:
 EcoRI; Plants were grown under six following different
 environmental regimes in greenhouse, Environment 1)
 240C/170C day/night, well-watered, with post-anthesis
 fertilizer, Environment 2) 240C/170C day/night,
 well-watered, without post-anthesis fertilizer,
 Environment 3) 370C/170C day/night, well-watered, with
 post-anthesis fertilizer, Environment 4) 370C/170C
 day/night, well-watered, without post-anthesis fertilizer,
 Environment 5) 370C/170C day/night plus drought, with
 post-anthesis fertilizer, Environment 6) 370C/170C
 day/night plus drought, without post-anthesis fertilizer,
 developing wheat grains from the following were excised
 1 at 3, 5, 7,
 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20,
 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12,
 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10,
 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by
 S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A
 cDNA library was made using poly (A) RNA, and the cDNA
 clones were in vivo excised to give pBlueScript SK(-)
 phageids in the Ty close lab (Chin, Close, Fenton) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (others)."

ORIGIN

Query Match 41.9%; Score 680.8; DB 5; Length 722;
 Best Local Similarity 97.6%; Pred. No. 7.6e-142;
 Matches 691; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 Db 41 GGCAGTATCAGTCTGTCTTCTCTCGAGATGCGCGGCAATGCGCGACGACAA 100
 15 GGCAGTATCAGTCTGTCTTCTCTCGAGATGCGCGGCAATGCGCGACGACAA 74
 QY 101 TGGTGAACCAAGAACCGCGCTCGCTCGTCAATGACAAAGAAATGGTATTTGGCGC 160
 Db 75 TGGTGAACCAAGAACCGCGCTCGCTCGTCAATGACAAAGAAATGGTATTTGGCGC 134
 QY 161 CGGTCCCTGAGGTGCTTCCCTTGGAGCTTCGAGCCCGGAGTCCAGAGGCTTGAATTC 220
 Db 135 CGGTCCCTGAGGTGCTTCCCTTGGAGCTTCGAGCCCGGAGTCCAGAGGCTTGAATTC 194
 QY 221 CAGCGAGGGCTGTGTCGACGCTGAGCTGTCCACGCGCCCGCGGTAG 280
 Db 195 CAGCGAGGGCTGTGTCGACGCTGAGCTGTCCACGCGCCCGCGGTAG 254
 QY 281 CGCGCAGCATGACGGGAAGCTTGCGCCGCGACGCTGCGACACCAAGTCCGACGCG 340
 Db 255 CGCGCAGCATGACGGGAAGCTTGCGCCGCGACGCTGCGACACCAAGTCCGACGCG 314
 QY 341 CGGCGAGGCGGCGCTCCAGAGGCCCAAGAGGCGGAAAAAGCCAAAGAGAGAGCTGA 400
 Db 315 CGGCGAGGCGGCGCTCCAGAGGCCCAAGAGGCGGAAAAAGCCAAAGAGAGAGCTGA 374

QY 401 GTCTGAGAAAGTGGAGGTCAAGATCGGCAACCCGCACTTGCGGCGGTGTGACGCGC 460
DB 375 GTCTGAGAAAGTGGAGGTCAAGATCGGCAACCCGCACTTGCGGCGGTGTGACGCGC 434
QY 461 CCATCGCGCGCGCGGTGTGAGAGCTTTTGTGGGCGCACTGAGAGCATCAGAGCGCAC 520
DB 435 CCATCGCGCGCGCGGTGTGAGAGCTTTTGTGGGCGCGGTGAGAGCATCAGAGCGCAC 494
QY 521 TGAATGTGGAGAGCTTCGCGCGCGCACTCAATGCGCGGGGTTTTCGGGTGATCATGAGGA 580
DB 495 TGAATGTGGAGAGCTTCGCGCGCGCACTCAATGCGCGGGGTTTTCGGGTGATCATGAGGA 554
QY 581 CGAAGGGGTGGCGCGCGCTCTTTCGCGCGCAACCGCGTCAACGTCCTCGGTCGCGCA 640
DB 555 CGAAGGGGTGGCGCGCGCTCTTTCGCGCGCAACCGCGTCAACGTCCTCGGTCGCGCA 614
QY 641 GCAAGGCGCATCGACATTTCACTTACGACACGCGGAAAGAAAGTACTTGAACCCGAGGCGC 700
DB 615 GCAAGGCGCATCGACATTTCACTTACGACACGCGGAAAGAAAGTACTTGAACCCGAGGCGC 674
QY 701 GCGAGCGCAGCGCAAGGTCCCATCCCGACGCGCGTCTGCGCGGAGCGC 748
DB 675 GCGAGCGCAGCGCAAGGTCCCATCCCGACGCGCGTCTGCGCGGAGCGC 722

RESULT 3
AM48477 856 bp mRNA linear EST 03-JAN-2001
LOCUS BRY 866 BRY Triticum aestivum cDNA clone P8-2A, mRNA sequence.
DEFINITION AM48477
VERSION AM48477.1 GI:12019012
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
1 (bases 1 to 856)
AUTHORS Clarke, B.C., Hobbs, M. and Appels, R.
TITLE Genes active in developing wheat endosperm
JOURNAL Unpublished (2000)
COMMENT Contact: Bryan Clarke
Division of Plant Industry
C.S.I.R.O.
GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Email: bryan@pl.csiro.au.

FEATURES
source 1..856
Location/Qualifiers

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/cultivar="Wynna"
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ORIGIN

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Best Local Similarity 92.6%; Pred. No. 5.5e-138;
Matches 786; Conservative 0; Mismatches 50; Indels 13; Gaps 8;
QY 14 GTGAGAGATGAAAGAACTCTAGGAGGAGCATATCAGTTCTGTCTTGTCTTCTGAG 73
DB 1 GTGAGAGATGAAAGAACTCTA-----GGCAGCATATCAGTTCTGTCTTCTGAG 55
QY 74 TGGCGGCGCAATGGCGCGAGCAATGCTGACCAAGAAACCGCGCTCGCTGCTCA 133
DB 56 TGGCGGCGCAATGGCGCGAGCAATGCTGACCAAGAAACCGCGCTCGCTGCTCA 115
QY 134 TGGACAAGAAAGAACTGGTTATTTGCGGCGGTCCCTGAGGTGCGCTTCCCTTGAGAGCTCGC 193

DB 116 TGGACAAGAAAGAACTGGTTCTTGTGCGGCGGTCCCTGAGGTGCGCTTCCCTTGAGAGCTCGC 175
QY 194 AGCCGAGATCAGAGAGCTTGAGATCTTCCAGCAAGGCTGTGTTGCCAGAGGTGAGACTCA 253
DB 176 AGCCGAGATCAGAGAGCTTGAGATCTTCCAGCAAGGCTGTGTTGCCAGAGGTGAGACTCA 235
QY 254 GCCGTGTCCACGCGCGCGCGCGGTAGCGCGAGCATGACGAGAAAGCTCGGCGCGC 313
DB 236 GCCGTGTCCACGCGCGCGCGCGGTAGCGCGAGCATGACGAGAAAGCTCGGCGCGC 295
QY 314 ACAGCTCGCAGCACAGCTTCGACGCGCGGCGAGCGGCGGTCCAGAAAGCCAGAA 373
DB 296 ACAGCTCGCAGCACAGCTTCGACGCGCGGCGAGCGGCGGTCCAGAAAGCCAGAA 355
QY 374 CGAAAAAGCGCAAAAGCGCAAGTGAATGTTGAGAAAGGTGAGAGGTCAATCGGCAAC 433
DB 356 CGAAAAAGCGCAAAAGCGCAAGTGAATGTTGAGAAAGGTGAGAGGTCAATCGGCAAC 415
QY 434 CGCACTGCGCGGCGGTGATGAGCGGCGCATCGCGGCGCGGTGTCAGAGACTTTCGTGG 493
DB 416 CGCACTGCGCGGCGGTGATGAGCGGCGCATCGCGGCGCGGTGTCAGAGACTTTCGTGG 475
QY 494 CGCACTGAGAGAGATCAGAGCGCACCTGATGTTGGGAGACTTCGCGCGCACTCAATGG 553
DB 476 CGCGCTGAGAGAGATCAGAGCGCACCTGATGTTGGGAGACTTCGCGCGCACTCAATGG 535
QY 554 CCGGGGTTTTCCGATGATCATCGGAGCGAGGGGTGGCGCGCTTTCGCGGCAACG 613
DB 536 CCGGGGTTTTCCGATGATCATCGGAGCGAGGGGTGGCGCGCTTTCGCGGCAACG 595
QY 614 CCGTCAACGTCCTCGCGGTGCGCGCAAGCGAGCGCATTCAGCACTTCACTTACGACA-CG 672
DB 596 CCGTCAACGTCCTCGCGGTGCGCGCGCAAGCGAGCGCATTCAGCACTTCACTTACGACA-CG 655
QY 673 GCGAAGAGTACTGACCCCGAGG-CGCGCGAGCGCAAGCGCAAGTCCCATCCCA-CGC 730
DB 656 GNCAGAAAGTACTGACCCCGAGGCGCGGCGAGCGCAAGCGCAAGTCCCATCCCA-CGC 715
QY 731 CGCTCGTCCCGGAGGCGCTGCG-CGAGTGGCGTCAACCTGTG-GCACTTATCCATGGA 788
DB 716 CGCTCGTCCCGGAGGCGCTGCGAGTGGCGCTTCAACCTGTGGGCACTTATCCATGGA 775
QY 789 GC-TGCTCAAGACCGGTCTCACCATGAGAA--GAGGTGATAGCAACCTCTCCACGC 845
DB 776 ACTTCTTAAGACCCCTCATCCATCAAGAAAGACGTTCCAAACCTCTCTCAGC 835
QY 846 GTTGTCAA 854
DB 836 GTTGTCAA 844

RESULT 4
BO609855 856 bp mRNA linear EST 25-JUN-2002
LOCUS BRY 866 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA
DEFINITION BO609855
ACCESSION BO609855.1 GI:21559194
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
1 (bases 1 to 856)
AUTHORS Clarke, B., Lambrecht, M. and Rhee, S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST
JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 12590341
PUBMED 12590341
COMMENT The Arabidopsis Information Resource

|||||
Db CGCGCCATCGCCGCGCGCTGTCAGAGACTTTGTGGCCGCACTGAGAGAGATCAGAGC 360
Qy 516 GCACCTGATGATGGTGGAGAGCTCCGCGCCGAGCTCCATATGGCGGGTTTCCGGTGGATCAT 575
Db 361 GCACCTGATGATGGTGGAGAGCTCCGCGCCGAGCTCCATATGGCGGGTTTCCGGTGGATCAT 420
Qy 576 GCGGACGAGAGGGGTGGCGCGGCTCTTCCGCGGCAAGCGCGTCAAGCTCCGCGCGGCG 635
Db 421 GCGGACGAGAGGGGTGGCGCGGCTCTTCCGCGGCAAGCGCGTCAAGCTCCGCGCGGCG 480
Qy 636 GCCAAGCAGAGCCATCGAGACCTTCACTTACGACACGCGCAGAGAGTACTGACCCCGA 695
Db 481 GCCAAGCAGAGCCATCGAGACCTTCACTTACGACACGCGCAGAGAGTACTGACCCCGA 540
Qy 696 GCGCGGAGACCGACCAAGGTCCCATCCGCGCGCTGTCGCGGAGCGCTCGCGG 755
Db 541 GCGCGGAGACCGACCAAGGTCCCATCCGCGCGCTGTCGCGGAGCGCTCGCGG 600
Qy 756 AGTGGCGTCAACCTGTGACCTATCCCATGAGAGCTGTCAAGACC 801
Db 601 AGTGGCGTCAACCTGTGACCTATCCCATGAGAGCTGTCAAGACC 646

RESULT 6
LOCUS CV054670 710 bp mRNA linear EST 24-AUG-2004
DEFINITION BNEB1124a Barley EST endospERM library Hordeum vulgare subsp. vulgare cDNA BNEB1124a 5' similar to putative Brittle-1 protein, chloroplast precursor, mRNA sequence.
ACCESSION CV054670
VERSION CV054670.1 GI:51517691
SOURCE EST.
ORGANISM Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
1 (bases 1 to 710)
Ali, S, Holloway, B. and Taylor, W.C.
Normalisation of cereal endospERM EST libraries for structural and functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 710.
Location/Qualifiers
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/cultivar="Himalaya"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="BNEB1124a"
/issue_type="endospERM"
/dev_stage="developing endospERM tissue 10, 12, 15 dpa (days post anthesis)"
/lab_host="DH10B (Life Technology)"
/note="Vector: Ziploxi; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endospERM tissues of the barley cultivar Himalaya. cDNA was synthesised from pooled 10, 12, and 15 dpa endospERM using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of Ziploxi vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

ORIGIN
Query Match 39.4%; Score 640.6; DB 7; Length 710;
Best Local Similarity 94.7%; Pred. No. 7,8e-133;
Matches 674; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
Qy 636 GCCAAGCAGAGCCATCGAGACCTTCACTTACGACACGCGCAGAGAGTACTGACCCCGA 695
Db 1 GCCAAGCAGAGCCATCGAGACCTTCACTTACGACACGCGCAGAGAGTACTGACCCCGA 60
Qy 696 GCGCGGAGCCAGCCAGAGGTCCCATCCGCGCGCTGTCGCGGAGCGCTCGCGG 755
Db 61 GCGCGGAGCCAGCCAGAGGTCCCATCCGCGCGCTGTCGCGGAGCGCTCGCGG 120
Qy 756 AGTGGCGTCAACCTGTGACCTATCCCATGAGAGCTGTCAAGACCCTGTCAACATCA 815
Db 121 AGTGGCGTCAACCTGTGACCTATCCCATGAGAGCTGTCAAGACCCTGTCAACATCA 180
Qy 816 GAAGAGCTGTACGACCAACCTCTCCAGCGGTTCTCAAGATGTCGCGAGAGAGCC 875
Db 181 GAAGAGCTGTACGACCAACCTCTCCAGCGGTTCTCAAGATGTCGCGAGAGAGCC 240
Qy 876 GCGGAGCTGTACCGCGGCTGCGCGCGAGCTGATCGCGTGTGTCCTGATCGCGGCG 935
Db 241 GCGGAGCTGTACCGCGGCTGCGCGCGAGCTGATCGCGTGTGTCCTGATCGCGGCG 300
Qy 936 CAACCTTCTACGCTTACGAGACGCTGCGCGCGCTGTACCGCGCGCTCGGGAAGAGCA 995
Db 301 CAACCTTCTACGCTTACGAGACGCTGCGCGCGCTGTACCGCGCGCTCGGGAAGAGCA 360
Qy 996 GGTGGGCAACGCTCCGAGCGCTGATCGGGTCCGGGGGGGGCCATAGCCAGCACCGG 1055
Db 361 GGTGGGCAACGCTCCGAGCGCTGATCGGGTCCGGGGGGGGCCATAGCCAGCACCGG 420
Qy 1056 CACGTTCCCGCTGAGAGTGGCGCGAGAGATGCAAGTGGCGCGTGGCGGAGGCA 1115
Db 421 CACGTTCCCGCTGAGAGTGGCGCGAGAGATGCAAGTGGCGCGTGGCGGAGGCA 480
Qy 1116 GGTGTCAAGAACGCTGCTGACGCGCATGTACTGTCTCTGAGAGAGAGGCAACCCCGG 1175
Db 481 GGTGTCAAGAACGCTGCTGACGCGCATGTACTGTCTCTGAGAGAGAGGCAACCCCGG 540
Qy 1176 GCTCTACCGCGGCTGCGCGCGCCAGCGCATCAAGCTCAAGCCCGCGCGCATCTCTT 1235
Db 541 GCTCTACCGCGGCTGCGCGCGCCAGCGCATCAAGCTCAAGCCCGCGCATCTCTT 600
Qy 1236 CATGTCTCTACGAGCGCTGCAAGAGATCTTGTGACGAGAAAGAGACGCGCGCGG 1295
Db 601 CATGTCTCTACGAGCGCTGCAAGAGATCTTGTGACGAGAAAGAGACGCGCGCGG 657
Qy 1296 CGAGCCCGAG 1347
Db 658 CGAGCCCGAG 709

RESULT 7
LOCUS AM448382 787 bp mRNA linear EST 03-JAN-2001
DEFINITION BRY 646 BRY Triticum aestivum cDNA clone P40-2D, mRNA sequence.
ACCESSION AM448382
VERSION AM448382.1 GI:12018917
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
1 (bases 1 to 787)
Clarke, B.C., Hobbs, W. and Apple, R.
Genes active in developing wheat endospERM
Unpublished (2000)
Contact: Bryan Clarke
Division of Plant Industry

C.S.I.R.O.
GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Email: bryan@p1.csiro.au.

FEATURES

source

Location/Qualifiers
1. .787

/organism="Triticum aestivum"
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/cultivar="Wynna"
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ORIGIN

Query Match 39.4%; Score 639.6; DB 2; Length 787;
Best Local Similarity 93.7%; Pred. No. 1.3e-132;
Matches 688; Conservative 0; Mismatches 44; Indels 2; Gaps 2;

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DB 1 GAAGAACTCTAGGAGGAGGCACTATCAGTTCTGTCTTCCGAGATGGGGGGC 60
OY 84 AATGGCCGCGACGACAAATGTGTACCAAGAACACCGCGCTCGCTGTATGACAAGAA 143
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OY 204 CAGAGGCTTGGAGCTTCCGACGAGGGGCTGTGTGGCGAGCGTGGGAGTCAAGCTGTCCA 263
DB 181 CAGAGGCTTGGAGCTTCCGACGAGGGGCTGTGTGGCGAGCGTGGGAGTCAAGCTGTCCA 240
OY 264 CGGCGCCCGCGCGGTAGGCGCGACATGACGAGAAAGGCTCGCGCCCGCGACGACGTGCG 323
DB 241 CGGCGCCCGCGCGGTAGGCGCGACATGACGAGAAAGGCTCGCGCCCGCGACGACGTGCG 300
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DB 301 ACACCAAGCTCGAGCGCGCGCGAGGCGCGGTCCAGAAAGGCCAGAAAGCGAAAGAGGC 360
OY 384 CAAAAGAGAGAGAGAGAGTGAAGAGAGAGTCAAGATCGGCAACCGGCAACCTGCG 443
DB 361 CAAAAGAGAGAGAGAGAGTGAAGAGAGAGTCAAGATCGGCAACCGGCAACCTGCG 420
OY 444 GCGGCTGTGACGCGCGCGCATCGCGCGCGGTGTGAGAGCTTTCGTGCGCGCACTGGA 503
DB 421 GCGGCTGTGACGCGCGCGCATCGCGCGCGGTGTGAGAGCTTTCGTGCGCGCACTGGA 480
OY 504 GACGATCAGACGACCTGTATGTGGGAGCTCCGCGCGCGCATCTCATAGCCGCGGGTTT 563
DB 481 GACGATCAGACGACCTGTATGTGGGAGCTCCGCGCGCGCATCTCATAGCCGCGGGTTT 540
OY 544 CCGGTGTGATCATGCGGAGAGAGGGTGGCCCGGCTCTTCCGCGCGCAACGCGCTCAAGT 623
DB 541 TCGGTGTGATCATGCGGAGAGAGGGTGGCCCGGCTCTTTCGCGGAAAGCGCGTCAAGT 600
OY 624 CTTCCGCTCGGCGCAAGAGGCGCATGAGC-ACCTCATTATGACACGCGGAGAAAGT 682
DB 601 CTTCCGCGGCGCGCGGCGGAGGCGCATGAGCACTTATCTTACACGCGGAGAAAGG 660
OY 683 ACCTGACCCCGAGAGC-CGCGAGGCGAGCAGAGTCCCATGCCACGCGCTGTGCGC 741
DB 661 ACCTGACCCCGAGAGCCTCGGAGAGCGCGGCAAGGCCGCCCATGCCATGCTTTTGC 720
OY 742 GAGGCGCTGCGCGG 755
DB 721 CGGAGCTTTCGCG 734

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RESULT 8

B0609766 787 bp mRNA linear EST 25-JUN-2002
LOCUS B0609766
DEFINITION BRY_646 wheat EST endosperm library Triticum aestivum CDNA 5', mRNA
sequence.

ACCESSION B0609766
VERSION B0609766
KEYWORDS B0609766.1 GI:21559105
SOURCE EST.
ORGANISM Triticum aestivum (bread wheat)

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 787)
Arabidopsis genomic information for interpreting wheat EST
sequences

JOURNAL Func. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PubMed 12590341

COMMENT

Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhe@acoma.stanford.edu.

FEATURES

source

Location/Qualifiers
1. .787

/organism="Triticum aestivum"
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/db_xref="taxon:4565"
/tissue_type="endosperm"
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(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN

Query Match 39.4%; Score 639.6; DB 5; Length 787;
Best Local Similarity 93.7%; Pred. No. 1.3e-132;
Matches 688; Conservative 0; Mismatches 44; Indels 2; Gaps 2;

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OY 24 GAAGAACTCTAGGAGGAGGCACTATCAGTTCTGTCTTCCGAGATGGGGGGC 83
DB 1 GAAGAACTCTAGGAGGAGGCACTATCAGTTCTGTCTTCCGAGATGGGGGGC 60
OY 84 AATGGCCGCGACGACAAATGTGTACCAAGAACACCGCGCTCGCTGTATGACAAGAA 143
DB 61 AATGGCCGCGACGACAAATGTGTACCAAGAACACCGCGCTCGCTGTATGACAAGAA 120
OY 144 GAAGCTGTATTATTTGGGGGGGGTCCCTGAGGTGCGCTTCCCTTGGAGCTGCAAGCCGAGT 203
DB 121 GAAGCTGTATTATTTGGGGGGGGTCCCTGAGGTGCGCTTCCCTTGGAGCTGCAAGCCGAGT 180
OY 204 CAGAGGCTTGGAGCTTCCGACGAGGGGCTGTGTGGCGAGCGTGGGAGTCAAGCTGTCCA 263
DB 181 CAGAGGCTTGGAGCTTCCGACGAGGGGCTGTGTGGCGAGCGTGGGAGTCAAGCTGTCCA 240
OY 264 CGGCGCCCGCGCGGTAGGCGCGACATGACGAGAAAGGCTCGCGCCCGCGACGACGTGCG 323
DB 241 CGGCGCCCGCGCGGTAGGCGCGACATGACGAGAAAGGCTCGGACCGCGCGACGACGTGCG 300
OY 324 ACACCAAGCTCGAGCGCGCGCGAGGCGCGGTCCAGAAAGGCCAGAAAGCGAAAGAGGC 383
DB 301 ACACCAAGCTCGAGCGCGCGCGAGGCGCGGTCCAGAAAGGCCAGAAAGCGAAAGAGGC 360
OY 384 CAAAAGAGAGAGAGAGTGAAGAGAGAGTCAAGATCGGCAACCGGCAACCTGCG 443
DB 361 CAAAAGAGAGAGAGAGTGAAGAGAGAGTCAAGATCGGCAACCGGCAACCTGCG 420
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Db 421 GCGGCTGCTAGCGGCGCCCATTTGCCGCGCCGCTGTGAGAGACTTTTGTGTGCTGCACCTGA 480
QY 504 GAGCATCAGACGACCTGATGTGTGGAGAGCTCGGCGCCGACTCATGTGCGCGGTTT 563
Db 481 GAGGATAGAGACGACCTGATGTGTGGAGAGCTCGGCGCCGACTCATGTGCGCGGTTT 540
QY 564 CCGGTGATCATGTGCGAGCGAGGGGTGCGCGCTTTCGCGGCAACGCGCTCAAGT 623
Db 541 TCGGTGATCATGTGCGAGCGAGGGGTGCGCGCTTTCGCGGCAACGCGCTCAAGT 600
QY 624 CTTCCCGGTGCGCGCAAGGAGGCTGAGC-ACCTCATCTTACGACAGCGCGAAGAGT 682
Db 601 CTTCCCGGTGCGCGCAAGGAGGCTGAGC-ACCTCATCTTACGACAGCGCGAAGAGT 660
QY 683 ACCTGACCCCGGAGGCG-CGCGAGCCGACGAGGAGGCTTCCGCGGCAACGCGCTGAGC 741
Db 661 ACCTGACCCCGGAGGCGCTGAGGAGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 742 GAGCGCTGCGCGG 755
Db 721 CGGACGCTTCCCG 734

RESULT 9
BQ608893 686 bp mRNA linear EST 25-JUN-2002
LOCUS BR1 4808 wheat EST endospem library Triticum aestivum cDNA 5',
DEFINITION mRNA sequence.
ACCESSION BQ608893.1 GI:21558232
VERSION BQ608893
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 686)
REFERENCE Clarke,B., Lambrecht,M. and Rhee,S.Y.
Arabidopsis genomic information for interpreting wheat EST
sequences
JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
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260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@coma.stanford.edu.

FEATURES
source
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/cultivar="Wyuha"
/db_xref="taxon:4565"
/rname_type="endospem"
/dev_stage="developing endospem tissue 8, 10 and 12 DPA
(days post anthesis)"
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Best Local Similarity 92.9%; Freq. No. 2e-122;
Matches 632; Conservative 0; Mismatches 46; Indels 2; Gaps 1;

QY 26 AGAATCTCAGGAGGAGGAGGATGATGCTGCTGCTGCTGAGATGCGCGGCA 85
Db 1 AGAATCTCAGGAGGAGGAGGATGATGCTGCTGCTGCTGAGATGCGCGGCA 60
QY 86 TGGCCGCGAGAGACATGTGTGATCCAGAGAACACCGCGCTGCTGATGAGCAAGAG 145
Db 61 TGGCCGCGAGAGACATGTGTGATCCAGAGAACACCGCGCTGCTGATGAGCAAGAG 120

QY 146 ACTGTTATTGCGGCGCGTCCCTGAGGTGCGCTTCCCTTGAGAGCTCGAGCCGAGTCA 205
Db 121 ACTGTTATTGCGGCGCGTCCCTGAGGTGCGCTTCCCTTGAGAGCTCGAGCCGAGTCA 180
QY 206 GAGCTTGAATCTTCCAGCGAGGAGCTGTTGTGCGCAGCGTGGAGCTGAGCTGTCCAG 265
Db 181 GAGCTTGAATCTTCCAGCGAGGAGCTGTTGTGCGCAGCGTGGAGCTGAGCTGTCCAG 240
QY 266 GCGCCCGCGGTGAGGCGCGGAGACATGACGCGGAAAGGTGCGGCGCGCGAGAGCTGCGAC 325
Db 241 GCGCCCGCGGTGAGGCGCGGAGACATGACGCGGAAAGGTGCGGCGCGCGAGAGCTGCGAC 300
QY 326 ACCAGCTGCGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 385
Db 301 ACCAGCTGCGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 386 AAAAGCAGCAGCTGAGTCTGAGAGAGGTGAGAGGTCAAGATCGGCAACCGCACTGCGGC 445
Db 361 AAAAGCAGCAGCTGAGTCTGAGAGAGGTGAGAGGTCAAGATCGGCAACCGCACTGCGGC 420
QY 446 GGTGCTGAGCGCGCGCATGCGCGCGCGGTGCGAGAGCTTTCGCGCGCACTGAGAG 505
Db 421 GGTGCTGAGCGCGCGCATGCGCGCGCGGTGCGAGAGCTTTCGCGCGCGCGCGCGCG 480
QY 506 CGATCAGAGCAGCAGCTGAGTGTGGAGAGCTCCGCGCGCGCATGCGAGCGCGCGCGGTTTCC 565
Db 481 CGATCAGAGCAGCAGCTGAGTGTGGAGAGCTCCGCGCGCGCATGCGAGCGCGCGGTTTCC 540
QY 566 GGTGATCATGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 623
Db 541 GGTGATCATGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 624 CTTCCCGGTGCGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 683
Db 601 CTTCCCGGTGCGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 684 CCGAGCCCGGAGGCGCGG 703
Db 661 CCGAGCCCGGAGGCGCGG 680

RESULT 10
AL506887 700 bp mRNA linear EST 04-JAN-2001
LOCUS AL506887 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone HY04115T 5', mRNA
sequence.
ACCESSION AL506887.1 GI:12033102
VERSION AL506887
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 700)
REFERENCE Michalek,W., Weschke,W., Pleisner,K.-P. and Graner,A.
Triticum aestivum L. EST sequencing and analysis in barley
JOURNAL Unpublished (2000)
COMMENT Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5' end.
Location/Qualifiers
1..700
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/mol_type="mRNA"
/cultivar="Barke"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HY04115T"

/lissue type="developing caryopsis (3.-15.DAP)"
 /lab host="XLOLR"
 /clone lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"
 /note="Vector: plasmid pBK-CMV, Site 1: EcoRI, Site 2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'- and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"

ORIGIN

Query Match 36.5%; Score 593.4; DB 1; Length 700;
 Best Local Similarity 92.0%; Pred. No. 3e-122;
 Matches 668; Conservative 0; Mismatches 29; Indels 29; Gaps 3;

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OY 32 CCTAGGCGGCACTATCACTTCTGTTCTTCTTCTGAGATGCGCGGCATATGCGG 91
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DB 2 CCTAGGCGGCACTATCACTTCTGTTCTTCTTCTGAGATGCGCGGCATATGCGT 61
    |||||
OY 92 CGACGACATGATGATCAAGAACAAACGCGCTCGCTCATGAGACAAAGAACTGGT 151
    |||||
DB 62 CACGACATGATGATCAAGAACAAACGCGCTCGCTCATGAGACAAAGAACTGGT 121
    |||||
OY 152 TATTCGCGCGGATCCCTGAGGTCCGCTTCCCTTGGAGTCCAGCGCGAGTCCAGAGCT 211
    |||||
DB 122 TCTTTCGCGCGGCTCTGAGGTCCGCTTCTTGGAGTCCAGCGCGAGTCCAGAGCT 181
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OY 212 TGGACTTCCACGCGAGGCTCTGTTCCGACGCTGGACCTAGCTCTGTTCCACGCGCGCC 271
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DB 182 TGGAGTTCCACGCGAGGCTCTGTTCCGACGCTGGACCTAGCTCTGTTCCAC----- 234
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OY 272 CGCGCGTATGCGCGAGATGACGCGGAAGGCTCGGCGCGCGACGACGCTCCGACACCGC 331
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DB 235 -----GACGCGAAGGCTCGGCGCGCGCGCGCGACGACGCTCCGACACCGC 274
    |||||
OY 332 TCGACGCCGCGGCGAGGCGGCGCTCCAGAAAGGCCAGAAAGCGAAGAAAGCCAAAGAGC 391
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DB 275 TCGACGCCGCGGCGAGATGCGGCGCTCCAGAGGCCAGAAAGCGAAGAAAGCCAAAGAGC 334
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OY 392 AGCAGCTAGTCTGAGGAAGGTGAGGCTCAAGATCGGCAACCCGCACTCGCGGCGCTGG 451
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DB 335 AGCAGCTAGTCTGAGGAAGGTGAGGCTCAAGATCGGCAACCCGCACTCGCGGCGCTGG 394
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OY 452 TCAGCGGCGCATCGCGCGCGCGCTGTCAGAGACTTGTGAGCGCACTGGAGACGATCA 511
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DB 395 TCAGCGGCGCATCGCGCGCGCGCTTTCNAGAGACTTGTGAGCGCGCTGGAGACGATCA 454
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OY 512 GAGACCACTGATGATGAGGAGCTTCGCGCGCACTCCATGAGCCGCGGCTTTTCGCGTGA 571
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DB 455 GAGACCACTGATGATGAGGAGCTTCGCGCGCACTCCATGAGCGCGGCTTTTCGCGTGA 514
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DB 515 TCATTCGAGCGAGGAGGCTTCGCGCGCTTTCGCGCGCAAGCGCGTCAAGCTCTCCGCG 574
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DB 575 TCAGCGCGCAAGAGCGCATTCAGACCTTCAGACGAGCGAGAAAGTAACTGAGACCC 634
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DB 695 CGCGCG 700
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RESULT 11

AL507153 700 bp mRNA linear EST 04-JAN-2001
 AL507153 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)

LOCUS

Hordeum vulgare subsp. vulgare cDNA clone HY05M09T 5', mRNA
 sequence.

ACCESSION

AL507153 GI:12033368

VERSION

AL507153

KEYWORDS

EST.

SOURCE

Hordeum vulgare subsp. vulgare

ORGANISM

Hordeum vulgare subsp. vulgare

REFERENCE

1. (bases 1 to 700)
 Michael, W., Meschke, W., Pleisner, K.-P. and Graner, A.

AUTHORS

EST sequencing and analysis in barley

TITLE

Unpublished (2000)

JOURNAL

Contact: Michael W

COMMENT

Institute for Plant Genetics and Crop Plant Research

FEATURES

Corrensstr. 3, D-06466 Gatersleben, Germany

source

Email: michael@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de

Location/Qualifiers

Seq primer: T3 primer for 5' end.

1. 700

/organism="Hordeum vulgare subsp. vulgare"

/mol type="mRNA"

/cultivar="barke"

/sub species="vulgare"

/db_xref="taxon:112509"

/clone="HY05M09T"

/lissue type="developing caryopsis (3.-15.DAP)"

/lab host="XLOLR"

/clone lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"

/note="Vector: plasmid pBK-CMV, Site 1: EcoRI, Site 2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'- and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"

ORIGIN

Query Match 36.4%; Score 592.2; DB 1; Length 700;
 Best Local Similarity 92.0%; Pred. No. 5.5e-122;
 Matches 668; Conservative 0; Mismatches 29; Indels 29; Gaps 3;

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OY 22 CTGAAGAACTCTAGGCGGCGACGATATCA-GTTCTGTTCTTCTTCTTCTGAGATGCGCGC 80
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DB 2 CTGAAGAACTCTAGGCGGCGACGATATCAAGTTCTGTTCTTCTTCTTCTGAGATGCGCGC 61
    |||||
OY 81 GGCATATGCGCGACGACATATGATGACCAAGAACACCGGCGCTCGCTGCTCATGAGCAA 140
    |||||
DB 62 GGCATATGCGCGACGACATATGATGACCAAGAACACCGGCGCTCGCTGCTCATGAGCAA 121
    |||||
OY 141 GAAGAACTGTTATGCGCGCGGATCCCTGAGTTCGCTTCTTGAAGCTCGAGCGCGCA 200
    |||||
DB 122 GAAGAACTGTTATGCGCGCGGATCCCTGAGTTCGCTTCTTGAAGCTCGAGCGCGCA 181
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OY 201 GTCCAGAGAGTTGAGTCTCCACGCGAGGCTCTGTTCCAGAGTGGAGACTAGCGCTGTC 260
    |||||
DB 182 GTCCAGAGAGTTGAGTCTCCACGCGAGGCTCTGTTCCAGAGTGGAGACTAGCGCTGTC 241
    |||||
OY 261 CCACGCGCGCGCGGATGCGCGCGAGCATGACGCGGAAGGCTCGCGCGCGCGACGACGCT 320
    |||||
DB 242 CCAC-----GACGCGGAAGGCTCGCGCGCGCGCGACGACGCT 274
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OY	331	CGCACAACCAAGCTTCGACGCCGCGGGCGAGGCGGGCGTCCAGAAAGGCCAGAGGCGCAAAA	380
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OY	391	GCGCAAAAAGCAGCAGCTGAGTCTGAGAGAGGTGAGGGTCAGATCGCGCAACCCGCACTT	440
Db	335	GCGCAAGAAAGCAGACTGGTGGTCTGAGGAAAGGTGAGGGTCAGATCGGCAACCCGCACTT	394
OY	441	GCGGCGGCTGGTCAACGGCGCCATTCGCGCGCCCGTGTGAGAGACTTTGTGGCGCACT	500
Db	395	GCGTGGCTGGTCACGCGCGCCATGCGCGCGCCCGTTTCAGAGACTTTGTGGCGCGCT	454
OY	501	GGAGACGATCAGAGCGCAGCACTTGATGGTGGAGACTTCGGCGCGCACTCCATGGCGGGGT	560
Db	455	GGAGAGCATCAGAGCGCACTGTGTTGGGAAGCTTCGGCGCGCACTCCATGGCGGGGT	514
OY	561	TTTCCGGTGGATCATGTCGGAGCGAGAGGGTGGCCCGGCTCTT-CCGCGGCAACGCGGTCA	619
Db	515	TTTCCGGTGGATCATGTCGGAGCGAGAGGGTGGCCCGGCTCTTCCGCGGCAACGCGGTCA	574
OY	620	ACGTCTCTCGCGTGGCGCGCAAGCAAGGCCATCGAGCACTTCACTTAACGACAGGGGAGGA	679
Db	575	ACGTCTCTCGCGTGGCGCGCAAGGAGGCCATCGAGCACTTCACTTAACGACAGGGGCAAGA	634
OY	680	AGTACCTGACCCCGGAGGCGCGGCGAGCCAGCCAGCAAGTCCCATTCGCCACGCCGCTCGTCG	739
Db	635	AGTACCTGACCCCGGAGGCGCGGCGAGCCAGCCAGCAAGTCCCATTCGCCACGCCGTTGTCG	694
OY	740	CCGGAG 745	
Db	695	CCGGAG 700	

RESULT 12
AL506597
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AL506597 700 bp mRNA linear EST 04-JAN-2001
AL506597 Hordeum vulgare Barke developing caryopsas (3.-15.DAP)
Hordeum vulgare subsp. vulgare cDNA clone HY03K09T 5', mRNA
sequence.
AL506597
AL506597.1 GI:12032812
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideaee; Triticeae; Hordeum.
1 (bases 1 to 700)
Michalek W., Meschke W., Pleisner K.-P. and Graner A.
EST sequencing and analysis in barley
unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michael@ipk-gatersleben.de, <http://pgrc.ipk-gatersleben.de>
Seq primer: T3 primer for 5' end.
Location/Qualifiers
1..700

by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb. Sequence trimming: Vector sequences and sequence ends were trimmed from the 5' and 3' end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp."

Query Match	35.6%	Score 577.8	DB 1	Length 700
Best Local Similarity	89.9%	Pred. No 9.4e-119		
Matches 653	Conservative 0	Mismatches 43	Indels 30	Gaps 2
Qy	8	GAGGGA	CTGAAGAACTCCTAAGCAGGGACGATACATTCTGTCTTCTCC	67
Db	1	GAGGGA	CTGAAGAACTCCTAAGCAGGGACGATACATTCTGTCTTCTCC	60
Qy	68	TCGAGATGGGGCGGCGCAATGGCCGCGACGACATGTGTGACCAAGAACACCCGGCCCTTCGC		127
Db	61	TCGAGATGGGGCGGCGCGCAATGTGTGACCAAGAACACCCGGCGCTTCGC		120
Qy	128	TCGTCATGAGCAAGAGAAACCTGTATTATTTGGGCGCGATCCCTGAGTGTGCTTCCCTTGA		187
Db	121	TCGTCATGAGCAAGAGAAACCTGTATTATTTGGGCGCGCTTGTGAGTGTGCTTCTTGA		180
Qy	188	GCTGCGACGCCCGAGTCCAGAGCTTTGACCTTCCACGACGAGGCTGTGTGCGACGCTGG		247
Db	181	GCTGCGACGCCCGAGTCCAGAGCTTTGACCTTCCACGACGAGGCTGTGTGCGACGCTGG		240
Qy	248	GACTCAGCTGTCCCAAGGCGCCCGCGGTAGCGCGACGATGATGGGAGGCTGTGGC		307
Db	241	GACTCAGCTGTCCCAAGGCGCCCGCGGTAGCGCGACGATGATGGGAGGCTGTGGC		273
Qy	308	CCGCGCAGCGACTTCGACACACAGCTTCGACCGCGCGGCGAGGCGGCGTCCAGAGGCC		367
Db	274	CCGCGCAGCGACTTCGACACACAGCTTCGACCGCGCGGCGAGTGGGCGTCCAGAGGCC		333
Qy	368	AGAGAGCGAAAAAGCCAAAAAGCAGACCTGATGCTGTAGAGAAAGTGAAGGCTAAGATCG		427
Db	334	AGAGAGCGAAAAAGCCAAAAAGCAGACCTGATGCTGTAGAGAAAGTGAAGGCTAAGATCG		393
Qy	428	GCAACCCGCGACTGGCGCGCGCTGATGAGCGGCGCGCATTCGCGCGCGCTTCAGAGACTT		487
Db	394	GCAACCCGCGACTGGCGCTGATGAGCGGCGCGCATTCGCGCGCGCTTCAGAGACTT		453
Qy	488	TGCTGGCGCGCACTGAGACGATCAGACGCACTGTATGTGTGGGAGGCTCCGCGCGCACT		547
Db	454	TGCTGGCGCGCGCTGAGACGATCAGACGCACTGTATGTGTGGGAGGCTCCGCGCGCACT		513
Qy	548	CCATGCGCGGGGCTTTTCGCTGATCATGTGGGACGAGAGGGGTGGCCCGGCTCTTCCGCG		607
Db	514	CCATGCGCGGGGCTTTTCGCTGATCATGTGGGACGAGAGGGGTGGCCCGGCTCTTCCGCG		573
Qy	608	GCAACGCGCTCAACGTCCTCGCGGTGCGCGCAAGCAAGGCGCATTCAGGACCTTCACTTACG		667
Db	574	GCAACGCGCTCAACGTCCTCGCGGTGCGCGCAAGGCGCATTCAGGACCTTCACTTACG		633
Qy	668	ACAACGCGGAAGTACTT---GACCCCGAGGCGCGCGAGCCAGGCAAGTCCCAATCC		724
Db	634	ACAACGCGGAAGTACTTGAACCCCGGAGGCGCGGCAAGCCAGCCAAAGGCTCCCA		693
Qy	725	CAACGC 730		
Db	694	TCCGCC 699		

RESULT 13					
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LOCUS	CD433626	897 bp	mRNA	linear	EST 03-JUN-2003
DEFINITION	EI01N0333C10.b Endosperm_3 Zea mays cDNA, mRNA sequence.				
ACCESSION	CD433626				
VERSION	CD433626.1	GI:31349269			
KEYWORDS	EST.				
SOURCE	Zea mays				

ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
Zea mays				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
1 (bases 1 to 897)				
Lai, J., Day, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkin, B., Bercraft, P. and Messing, J.				
Characterization of the maize endosperm transcriptome and its comparison to the rice genome				
Genome Res. 14 (10), 1932-1937 (2004)				
Contact: Lai, Jinsheung				
Dr. Joachim Messing's lab				
Waksman Institute, Rutgers University				
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA				
Tel: 732-445-3801				
Fax: 732-445-5735				
Email: jlai@waksman.rutgers.edu				
Seq primer: 73.				
FEATURES				
Source				
1..897				
/organism="Zea mays"				
/mol_type="mRNA"				
/culivar="W22"				
/db_xref="taxon:4577"				
/rissue_type="Endosperm of 7-23DAP"				
/clone_lib="Endosperm_3"				
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"				
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Query Match	35.3%	Score 573.6;	DB 6;	Length 897;
Best Local Similarity	84.3%;	Pred. No. 8.4e-118;		
Matches	661;	Conservative	0;	Mismatches 114;
			Indels	9;
			Gaps	1
395 AGCTAGTGTGAGGAAGTGAAGGTCGAATCGGCAACCGGACCTGGCGGCTGGTCA	454			
114 ATCTAGCCTGAGGAAGTCAAGGTCATAGATGCGCAACCGGACCTGGCGGCTGGTCA	173			
455 GCGGCGCCATCCCGCGCGCGCTGTGAGGACCTTTCGTGGCGGCATCTGAGAGCATGAGA	514			
174 GCGGCGCCATCCCGCGCGCGCTGTGAGGACCTTTCGTGGCGGCATCTGAGAGCATGAGA	233			
515 GCGACCTGATGTTGGGAGCTTCGGGCGCGACTCCATGCGCCGGGGTTTTCGGTGGATCA	574			
234 GGCATTTGATGCTCGCGAGCATCGGCTGACCTCCATGCGCGCGGGTTCAGTGATCA	293			
575 TGGCGAGCGAGGGGTGGCCCGGCTCTTCGCGGAGCAAGCGCTCAAGCGCTTCGCGGTCG	634			
294 TGCAGAACCAAGGGTGGAGCGGCGCTGTTCGCGGAGCAAGCGCTCAAGCGCTTCGCGGTCG	353			
635 GCGCAAGCAAGGCGCATTCAGACCTTCACTTACAGACAGCGGAGAAAGTACCTGACCCCG	694			
354 CTCGAGCAAGGCTTATCGACATTTTCACTTATGACAGCGGCAAGAGTTCTTACCCCA	413			
695 AGGCGGCGAGCGCAGCCAAAGTCCCATCCCAAGCGCGCTCGTCCGCGAGGCGCTGCGG	754			
414 AGGGCGAGCGAGCGCGCCAAAGTCCCATCCCAAGCGCGCTCGTCCGCGAGGCGCTGAGCGG	473			
755 GAGTGGCGTCAACCTCTGCGACCTTATCCATGAGAGGCTGCTCAAGACCGGCTTCAACATG	814			
474 GATTTGCGCTCAACCTTGTGACCTTATCCCATGAGTGTATCAAGACCAAGGGTTCACATG	533			
815 AGAAGGACGTGTACGACCACTCTTCAGCGGTTCTCAAGATCGTGGCGGAGCAAGGCGC	874			
534 AGAAGGACGTGTATACGACCACTCTTCAGCGGTTCTGTGAAGATCTTACCGGAGAGGGCC	593			
875 CGGCGGAGCTGTACCGCGGGCTTGCGCGCGAGCTGTATCGCGGTGTACCGTACGCGACG	934			
594 CGTCCGAGCTGTATCGTGGGCTTGACCAAGCGCTGTATCGCGGTGTACCGGTACGCGGCTT	653			
935 CCAACTTCTTACGCTTACGAGAGCGTGGCGCGGTGTACCGCGCGGCTGTGCGGG-----	987			
654 GTTAACTTCTTACGCTTACGAGAGCGCTGTACCGGTGTACCGGTGTACCGGCGGCGCTG	713			

Qy	988	--AAAGAGAGATGGGACAAAGTCCCGACGCTGTGAATCGGGGTCCGGGGCGGGGCCATAG	1045
Db	714	CCGGCGGGGAGAGTGGAGTGGAGCCCGTGGCGACGCTGTGCATCGGGATCCGGCGGGGCCATCG	773
Qy	1046	CCAGACAGGACCACTTCCCGCTGGAGGTGGCGGGAGACAGATGACAGTGGGCGCCGTGG	1105
Db	774	CCACTCGGCGCACTTCCCGCTAGAGGTGGCCGGCAAGAGATGACAGTGGGCGCTGGG	833
Qy	1106	GCGGGAGGACAGGTGTACAAAGACGTGCTGCACGCCATGTACTGATCTTGGAGAAGAGG	1165
Db	834	GCGGGAGGACAGGTGTACCAAGAACGTCTCCACGCTATCTACTGATCTCAAGAAAGG	893
Qy	1166	GCAC	1169
Db	894	GGCG	897
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LOCUS		linear	EST 24-JUL-2000
DEFINITION	BE413774	SCU002.H05.R990714 ITFC SCU wheat Endosperm library Triticum	
ACCESSION	BE413774	aestivum cDNA clone SCU002.H05, mRNA sequence.	
VERSION	BE413774.1	GI:9411620	
KEYWORDS	EST.		
SOURCE	Triticum aestivum (bread wheat)		
ORGANISM	Triticum aestivum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.		
AUTHORS	1 (bases 1 to 784)		
	Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Hermann,R.G., Holton,T., Jaccquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.V., McGuire,P., Ogden,R.Y., Pecchioni,N., Quiset,C., Schuch,W., Selvaraj,G., Shriver,M., Sorrells,M., Warburton,M. and Wenzel,G.		
TITLE	International Triticeae EST Cooperative (ITREC): Production of Expressed Sequence Tags for Species of the Triticeae		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Holton T		
	Centre for Plant Conservation Genetics, Southern Cross University		
	PO Box 157, Lismore NSW 2480 AUSTRALIA		
	Tel: 61 2 6620 3409		
	Fax: 61 2 6622 2080		
	Email: tholton@scu.edu.au		
	International Triticeae EST Cooperative (ITREC)		
	http://wheat.pw.usda.gov/genome.		
FEATURES	Location/Qualifiers		
SOURCE	1..784		
	/organism="Triticum aestivum"		
	/mol_type="mRNA"		
	/cultivar="Wyuna"		
	/db_xref="taxon:4565"		
	/clone="SCU002.H05"		
	/cruise_type="endosperm"		
	/clone_lib="ITREC SCU Wheat Endosperm Library"		
	/note="Vector: Bluescript II SK(-)"		
ORIGIN			
Query Match	34.4%;	Score 559.2;	DB 2; Length 784;
Best Local Similarity	94.7%;	Pred. No. 1.4e-114;	
Matches 627; Conservative	0; Mismatches 28; Indels 7; Gaps 5;		
Qy	156	GCGGCGGTCCTTAAGTCCGCTTTCCTTGGAGCTGCGAGCCGACAGTCCAGAGACTTGA	215
Db	125	GCGGCGGTCCTTAAGTCCGCTTTCCTTGGAGCTGCGAGCCGACAGTCCAGAGACTTGA	184
Qy	216	CTTCCACAGCAGGGCTGTTCGACAGGTGGAGCTAGACTGTCCACAGGCGCCCGCC	275
Db	185	CTTCCACAGCAGGGCTGTTCGACAGGTGGAGCTAGACTGTCCACAGGCGCCCGCC	244

QY 1375 ACTAGATGAAGCA-----TTATGGTGAACCGTCAAAATCAGAGAAATGCGTGAATT 1426
Db 614 ACGGATCGACGAGACATTTATGCATGGTTACCGTCAAAATCAGAGAAATGCGTGAATT 673
QY 1427 GAAATTTTGAAGTGTGAGCCTTATTCGATTTGAATCCTAAGCTGGAAGTG 1477
Db 674 GAA-TTTTCAAGTGTGAGCCTTGAATCTAAGGNGGAAAG 723

Search completed: May 25, 2005, 12:24:38
Job time : 8074 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 04:44:09 ; Search time 1311 Seconds
(without alignment)
7337.589 Million cell updates/sec

Title: US-10-659-199-17

Perfect score: 1625

Sequence: 1 ggcacgctgagggagtggaag.....aaaaaaaaaaaaaaaaaaaaa 1625

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

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- 2: geneeqn1990s:*
- 3: geneeqn2000s:*
- 4: geneeqn2001s:*
- 5: geneeqn2001bs:*
- 6: geneeqn2002as:*
- 7: geneeqn2002bs:*
- 8: geneeqn2003as:*
- 9: geneeqn2003bs:*
- 10: geneeqn2003cs:*
- 11: geneeqn2003ds:*
- 12: geneeqn2004as:*
- 13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	673.4	41.4	675	12	Adj42967 Plant CDN
2	672.6	41.4	1213	12	Adj40023 Plant CDN
3	549	33.8	698	12	Adj41898 Plant CDN
4	539.4	33.2	640	12	Adj42968 Plant CDN
5	511	31.4	661	12	Adj42969 Plant CDN
6	440.4	27.1	1056	12	Adj42974 Plant CDN
7	400.2	24.6	1267	2	Aaz20025 Wheat bti
8	397.6	24.5	1140	10	Aaz57636 Rice grai
9	392.6	24.2	449	2	Aaz20024 Wheat bti
10	361.6	22.3	1099	12	Adj42975 Plant CDN
11	357.8	22.0	1331	3	AAC49806 Arabidops
12	357.8	15.8	1334	3	AAC35455 Arabidops
13	256.8	15.6	829	3	Adj42973 Plant CDN
14	253.8	14.9	829	3	AAC49805 Arabidops
15	241.4	13.7	654	12	AAC34062 Arabidops
16	222.4	11.0	580	2	Adj44581 Plant CDN
17	179	8.1	523	12	Aaz20023 Soybean b
18	132	8.0	285	6	Abj44164 Plant CDN
19	129.8	7.8	3334	8	Abj3796 Corn tass
20	127				Acdd5177 Human sec

21	125.4	7.7	1481	3	AAC76538 Human ORF
22	125.4	7.7	3337	4	Aa159228 Human pol
23	125.4	7.7	3333	3	Aa65058 Membrane-
24	125.4	7.7	3334	4	AaF92086 Human PRO
25	125.4	7.7	3334	5	AaF44204 Human PRO
26	125.4	7.7	3334	6	Ab874406 Human CDN
27	125.4	7.7	3334	6	ACA64351 Novel hum
28	125.4	7.7	3334	8	ACA91192 Novel hum
29	125.4	7.7	3334	8	ACD81569 Human CDN
30	125.4	7.7	3334	8	ACA60391 Novel hum
31	125.4	7.7	3334	8	ACA58838 CDNA enco
32	125.4	7.7	3334	8	ACA64014 CDNA enco
33	125.4	7.7	3334	8	ACA91278 CDNA enco
34	125.4	7.7	3334	8	ABX80810 Human sec
35	125.4	7.7	3334	8	ACD44319 CDNA enco
36	125.4	7.7	3334	8	ACA93725 Human CDN
37	125.4	7.7	3334	8	ACA67299 CDNA enco
38	125.4	7.7	3334	8	ACH66272 Novel hum
39	125.4	7.7	3334	8	ABX79490 Human sec
40	125.4	7.7	3334	8	ACA93511 Novel hum
41	125.4	7.7	3334	8	ABX81193 Novel hum
42	125.4	7.7	3334	8	ACD02326 Novel hum
43	125.4	7.7	3334	8	ACA89317 Novel hum
44	125.4	7.7	3334	8	ACA68954 Novel hum
45	125.4	7.7	3334	8	ACA93009 Novel hum

ALIGNMENTS

RESULT 1	
ADJ42967	
ID	ADJ42967 standard; CDNA; 675 BP.
XX	
AC	ADJ42967;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Plant CDNA #3967.
XX	
KW	Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW	soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW	maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW	stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW	plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX	antifungal.
OS	
XX	Eukaryota.
PN	
XX	US2004016025-A1.
PD	
XX	22-JAN-2004.
PF	
XX	26-SEP-2002; 2002US-00260238.
PR	
XX	26-SEP-2001; 2001US-0325277P.
PR	26-SEP-2001; 2001US-0325448P.
PR	04-APR-2002; 2002US-0370620P.
XX	
PA	(BUDM) BUDMORTH P.
PA	(MOUG) MOUGHAMER T.
PA	(BRIG) BRIGGS S P.
PA	(COOP) COOPER B.
PA	(GLAZ) GLAZEBROOK J.
PA	(GOFF) GOFF S A.
PA	(KATA) KATAGIRI F.
PA	(KREP) KREPS J.
PA	(PROV) PROVART N.
PA	(RICK) RICE D.
PA	(ZHUT) ZHU T.
PI	Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F, Kreps J, Provart N, Rike D, Zhu T;

```
XX DR WPI; 2004-190374/18.
XX PT New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Example 13; SEQ ID NO 3967; 230pp; English.
XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX CC encode are useful for manipulating crop plants to alter or improve
XX CC phenotypic characteristics, to produce large quantities of oil or
XX CC proteins, to incur resistance to insecticides, viruses or fungi, and to
XX CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX CC have a high nutritional value with reduced apical dominance or dwarfism,
XX CC early flowering or altered metabolic pathways. This sequence represents a
XX CC plant nucleic acid of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification but was obtained in
XX CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 675 BP; 153 A; 176 C; 224 G; 122 T; 0 U; 0 Other;

Query Match      41.4%; Score 673.4; DB 12; Length 675;
Best Local Similarity 99.9%; Pred. No. 1.9e-119;
Matches 674; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 912 CGGCGTGTGCGCGTACCGGCGGCCAACTTCTACGCTTACGAGACGCTGCGCGCGTGA 971
Db 1 CGGCGTGTGCGCGTACCGGCGGCCAACTTCTACGAGACGCTGCGCGCGTGA 60

Qy 972 CGGCGCGCGCGTGGGGAAGAGAGGTGGGCAAGTCCGACGCTGCTGATCGGGTCCG 1031
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Qy 1032 GGGGGGGGCGCATGCGCGACGCGCAGTTCGCGTGGAGGTGGCGGGAAGCAGATGCA 1091
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Qy 1092 GGTGGGGCGCGTGGGCGGAGGCGAGTGTACAAAGACGTGTGACCGCCATGTACTGCAT 1151
Db 181 GGTGGGGCGCGTGGGCGGAGGCGAGTGTACAAAGACGTGTGACCGCCATGTACTGCAT 240

Qy 1152 CCTCTGAGAGAGAGGCGACCGCGCGGCTCTACCGCGGGCTCGGCCCGACGCTGATCAAGCT 1211
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Qy 1212 CATGCCGCGCGCGCGCATCTCTCATGTGTACGAGGCGCGAAGAGATCTGTGCA 1271
Db 301 CATGCCGCGCGCGCGCATCTCTCATGTGTACGAGGCGCGAAGAGATCTGTGCA 360

Qy 1272 CGAAGAAAGAGACGCGCGCGCGCGCGAGCCCGACGAGAGACGAGACCGGACGAGCG 1331
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Qy 1332 AGGACAGGCGCGCGCGCCCAAGAGCTGAAAGGTGATCGGCATGAACCTAGATCAATAT 1391
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Qy 1392 GGTGACCGTGAATTCGAGAAAGAAATGCTGATTTGAATTTTGAAGTGAAGCCCTAT 1451
Db 481 GGTGACCGTGAATTCGAGAAAGAAATGCTGATTTGAATTTTGAAGTGAAGCCCTAT 540

Qy 1452 TGCATTTGAATCTTAAGCTGGAAGTGGCGCCTTGAAGATTGATTTGTTGTTCAAGG 1511
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Db 541 TGCATTTGAATCTTAAGCTGGAAGTGGCGCCTTGAAGATTGATTTGTTGTTCAAGG 600
Qy 1512 AACATGTCGGTTTCAGTATGCGCGTGAATGATTTATGACACTTCTGTATCAATTC 1571
Db 601 AACATGTCGGTTTCAGTATGCGCGTGAATGATTTATGACACTTCTGTATCAATTC 660
Qy 1572 AATTAAGAAAGAACTC 1586
Db 661 AATTAAGAAAGAACTC 675

RESULT 2
ADJ40023
ID ADJ40023 standard; cDNA; 1213 BP.
XX ADJ40023;
XX AC
XX DT 06-MAY-2004 (first entry)
XX XX
DE Plant cDNA #1023.
XX
XX KM Plant; gene; seq; transcription; plant genome augmentation; cereal;
XX KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
XX KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
XX KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
XX KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX KM antifungal.
XX OS Eukaryota.
XX XX
XX PN US2004016025-A1.
XX XX
XX PD 22-JAN-2004.
XX XX
XX PF 26-SEP-2002; 2002US-00260238.
XX XX
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 26-SEP-2001; 2001US-0325448P.
XX PR 04-APR-2002; 2002US-0370620P.
XX XX
XX PA (BUDW/) BUDWORTH P.
XX PA (MOUG/) MOUGHAMER T.
XX PA (BRIG/) BRIGGS S P.
XX PA (COOP/) COOPER B.
XX PA (GLAZ/) GLAZEBROOK J.
XX PA (GOF/) GOF S A.
XX PA (KAT/) KATAGIRI F.
XX PA (KREP/) KREPS J.
XX PA (PROV/) PROVART N.
XX PA (RICK/) RICHE D.
XX PA (ZHU/) ZHU T.
XX XX
XX PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;
XX XX
XX DR WPI; 2004-190374/18.
XX PT New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Claim 25; SEQ ID NO 1023; 230pp; English.
XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
```

CC encode are useful for manipulating crop plants to alter or improve
 CC phenotypic characteristics, to produce large quantities of oil or
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
 CC have a high nutritional value with reduced apical dominance or dwarfism,
 CC early flowering or altered metabolic pathways. This sequence represents a
 CC plant nucleic acid of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1213 BP; 191 A; 419 C; 438 G; 165 T; 0 U; 0 Other;

Query Match 41.4%; Score 672.6; DB 12; Length 1213;
 Best Local Similarity 82.3%; Pred. No. 2.9e-119;
 Matches 825; Conservative 0; Mismatches 164; Indels 14; Gaps 4;

QY 291 TGACGGAGAGGCTGCGCCCGCCGACGACGTCGACACGACTTCGACGCCG----- 341
 DB 155 TGCGGCGAAGGGCGCGGACACTGCGACGTCGCGCGGCGACTCGCGCGGAGGCCGA 214
 QY 342 GGGCGAGGGCGGCGCTCCGAGAGGCCGAGAGGCGGAGGCGGCGGCGGCGCTGCTGTC 401
 DB 215 GAGAGCGGCGGAGAGAGAGGCGGCGGAGAGAGGAGGCGGCGGCGGCGCTGCTGTC 274
 QY 402 TCTGAGAGAGGTGAGGGGTCAAGATCGGACACCGGCGGCGGCTGTCAGCGCGC 461
 DB 275 GCTTGAAGAGGTGAGGGGTCAAGATCGGAGAGCGGACCTTCGCGGCTGTCAGCGCGC 334
 QY 462 CATCGCGGCGGCGCTGTCGAGAGACTTTCGTCGCGCGGCGGCGGCGGCGGCGGCGCT 521
 DB 335 CATCGCGGCGGCGGCTGTCGAGAGACTTTCGTCGCGCGGCGGCGGCGGCGGCGGCGCT 394
 QY 522 GATGTCGGGAGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 581
 DB 395 CATGTCGGGAGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 454
 QY 582 GAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 641
 DB 455 GAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 514
 QY 642 CAAGGCGCATC--GAGCACTTCACTTACGACAGCGGCGGAGAGAGTCTGAGCGCGGAGGCC 699
 DB 515 CAAGGCGCATCAGAGAGATTTCACGACAGCGGCGGAGAGAGTCTGAGCGCGGAGGCC 574
 QY 700 GCGGAGCGCAGGAGAGTCCCATTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 759
 DB 575 GCGGAGCGCTGCGCAAGATCCCATCCCGCTGCTGTCGCGGCGGCGGCGGCGGCGGCTGTC 634
 QY 760 GCGTCAACCTGTGACCTTACGAGTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 817
 DB 635 GCGTCAACCTGTGACCTTACGAGTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 694
 QY 818 AGGACGTGACGACAACTCTCTCAACGCGGCTTCAAGATCGTCGCGGAGAGCGCGCG 877
 DB 695 AGGACGTGACGACAACTCTCTCAACGCGGCTTCAAGATCGTCGCGGAGAGCGCGCG 754
 QY 878 GGGAGCTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 937
 DB 755 GGGAGCTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 914
 QY 938 ACTTCTACGCGTACGAGAGCTGCGCGCTGCTGACGCGGCGGCGGCGGCGGCGGCGGCT 996
 DB 815 ACTTCTACGCGTACGAGAGCTGCGCGCTGCTGACGCGGCGGCGGCGGCGGCGGCGGCT 874
 QY 997 GTGGGCAAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1056
 DB 875 GTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 934
 QY 1057 AGCTTCCGCTGAGAGTGGCGGCGGAGAGAGATGAGTGGCGGCGGCGGCGGCGGCGGCGGCT 1116
 DB 935 ACCTTCCGCTGAGAGTGGCGGCGGAGAGAGATGAGTGGCGGCGGCGGCGGCGGCGGCT 994
 QY 1117 GTGTACAAAGAGCTGTGACGCGCATGTACTGATCTCTGAGAGAGAGGCGGCGGCGG 1176

DB 995 GTGTACCGCCGACGTCCTCAAGCATGTGCACTTCCTCCGCGGAGGCGCGCGGCGGCGGCGGCGGCT 1054
 QY 1177 CTGTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1236
 DB 1055 CTGTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1114
 QY 1237 ATGTCTACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1279
 DB 1115 ATGTCTACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1157

RESULT 3

ADJ41898
 ID ADJ41898 standard; cDNA; 698 BP.

XX ADJ41898;

DT 06-MAY-2004 (first entry)

DE Plant cDNA #2898.

KM Plant; gene; ss; transcription; plant genome augmentation; cereal;
 KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KM antifungal.

OS Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004.

XX 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.

PR 26-SEP-2001; 2001US-0325448P.

PR 04-APR-2002; 2002US-0370620P.

XX (BUDW/) BUDWORTH P.

PA (MOUG/) MOUGHAMER T.

PA (BRIG/) BRIGGS S. P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOLF/) GOLF S. A.

PA (KATR/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (PROV/) PROVART N.

PA (RICK/) RICE D.

PA (ZHUT/) ZHU T.

PI Budworth P., Moughamer T., Briggs S.P., Cooper B., Glazebrook J.,

PI Goff S.A., Katagiri F., Kreps J., Provart N., Riche D., Zhu T.,

XX WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
 PT improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.

PS Example 13; SEQ ID NO 2898; 230bp; English.

XX The invention relates to plant nucleotide sequences that direct seed-,
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
 CC or constitutive transcription of an operatively linked nucleic acid
 CC segment. The invention also relates to a method for augmenting a plant
 CC genome and a method of identifying a gene, where its expression is
 CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 698 BP, 125 A; 224 C; 241 G; 108 T; 0 U; 0 Other;

Query Match 33.8%; Score 549; DB 12; Length 698;

Best Local Similarity 92.7%; Pred. No. 1.2e-95;

Matches 600; Conservative 0; Mismatches 40; Indels 7; Gaps 2;

```
QY 4 CAGTGAAGAGTGAAGACTGAGAACTCTTGGCAGGGGCGATGATCACTTGTCTTCC 63
DB 1 CAGTGAAGTGAAGTGAAGACTGAGAACTCTTGGCAGGGGCGATGATCACTTGTCTTCC 55
QY 64 TTCTCGAGATGGGGGGGCGCAATGGCGCGACGCAATGGTGAACAAACCGGGCC 123
DB 56 TTCTCGAGATGGGGGGGCGCAATGGCGCGACGCAATGGTGAACAAACCGGGCC 115
QY 124 TTCTCGATGAGCAAGAAAGTGTATTGCGCGCGCTCTTGAAGTCTGCTTCCCT 183
DB 116 TTCTCGATGAGCAAGAAAGTGTATTGCGCGCGCTCTTGAAGTCTGCTTCCCT 175
QY 184 TGGAGCTGCGAGCCGCGAGTCCAGAGCTTGGACTTCCACGCGAGGCTCTGTTCCAGC 243
DB 176 TGGAGCTGCGAGCCGCGAGTCCAGAGCTTGGACTTCCACGCGAGGCTCTGTTCCAGC 235
QY 244 GTGGAGCTCAGCCGTCTCCACGCGCGCGCGGTGACGCGCGAGCAATGACGGAGAGCT 303
DB 236 GTAGAGCTCAGCCGTCTCCACGCGCGCGCGGTGACGCGCGAGCAATGACGGAGAGCT 295
QY 304 CGGCGCGCGCGAGCTGCGACACAGCTCGACGCCCGCGCGAGGCGGCGTCCAGAG 363
DB 296 CGGCGCGCGCGAGCTGCGACACAGCTCGACGCCCGCGCGAGGCGGCGTCCAGAG 355
QY 364 GCCCAGAGGCGGAGGCGGAGGCGGAGGCGAGCTGAGTGTGAGAGAGTGAAGGCTCAG 423
DB 356 GCCCAGAGGCGGAGGCGGAGGCGGAGGCGAGCTGAGTGTGAGAGAGTGAAGGCTCAG 415
QY 424 ATGCGCAACCGCGACCTGCGCGCGCTGTGACGCGCGCGCAATGCGCGCGCTGTGAGG 483
DB 416 ATGCGCAACCGCGACCTGCGCGCGCTGTGACGCGCGCGCAATGCGCGCGCTGTGAGG 475
QY 484 ACTTCGTGGGCGCACTGAGACGATCAGACGCACTGATGTGAGGAGGCTCGGCGCC 543
DB 476 ACTTCGTGGGCGCGCTGAGACGATCAGACGCACTGATGTGAGGAGGCTCGGCGCC 535
QY 544 GACTCCATGCGCGGGGTTTTCGGGTGATCATGCGGAGCGAGGGGTGCGCGCTTTC 603
DB 536 GACTCCATGCGCGGGGTGTTTTCGGGTGATCATGCGGAGCGAGGGGTGCGCGCTTTC 593
QY 604 CGCGGCAACCGCGTCAACGTCTCGGCTCGGCGCGCAAGGCGCAT 650
DB 594 CGCGGCAACCGCGTCAACGTCTCGGCTCGGCGCGCAAGGCGCTCGGCGCTT 640
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RESULT 4

ADJ42968

ID ADJ42968 standard; cDNA; 640 BP.

XX ADJ42968;

AC

DT 06-MAY-2004 (first entry)

XX Plant cDNA #3968.

DE

XX Plant; gene; ss; transcription; plant genome augmentation; cereal;

KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.

OS Eukaryota.

XX US2004016025-A1.

XX

XX 22-JAN-2004.

XX 26-SEP-2002; 2002US-00260238.

XX 26-SEP-2001; 2001US-0325277P.

XX 26-SEP-2001; 2001US-0325448P.

XX 04-APR-2002; 2002US-0370620P.

XX (BUDW/) BUDWORTH P.

XX (MOUG/) MOUGHAMER T.

XX (BRIG/) BRIGGS S P.

XX (COOP/) COOPER B.

XX (GLAZ/) GLAZEBROOK J.

XX (GOF/) GOF S A.

XX (KATA/) KATAGIRI F.

XX (KREP/) KREPS J.

XX (PROV/) PROVART N.

XX (RICK/) RICHKE D.

XX (ZHU/) ZHU T.

XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;

XX Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;

XX WPI; 2004-190374/18.

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Sequence 640 BP, 152 A; 172 C; 199 G; 117 T; 0 U; 0 Other;

Query Match 33.2%; Score 539.4; DB 12; Length 640;

Best Local Similarity 94.2%; Pred. No. 8.4e-94;

Matches 619; Conservative 0; Mismatches 21; Indels 17; Gaps 5;

```
QY 942 CTACGCTTACGAGAGCGTGGCGGCGTGTACCGCGCGGCGGAGAGAGAGGTGG 1001
DB 1 CTACGCTTACGAGAGCGTGGCGGCGTGTACCGCGCGGCGGAGAGAGAGGTGG 59
QY 1002 CAACGTCCGACCGCTGTGTCGGGTCCGGGCGGCGCCATGACGACGCGCCACGTT 1061
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Db 60 CAACGTGCGACGCTCTGATC-GGTCCGCGCGCGGCCCATAGCCAGCACCCGACGTT 118
 QY 1062 CCCGCTGAGGTGGGCGGAGAGCATGACGTTGGGCGCGTGGGGGAGGAGGATGTA 1121
 Db 119 CCGCTGGAGGTGGCGGAGAGCATGACGTTGGGCGCGTGGGGGAGGAGGATGTA 178
 QY 1122 CAAGAACGTGCTGACGCGCATGCTACTGATCTCTGAGAAAGAGGAGCGCGGGCTCTA 1181
 Db 179 CAAGAACGTGCTGACGCGCATGCTACTGATCTCTGAGAAAGAGGAGCGCGGGATCTTA 238
 QY 1182 CCGCGGCTCGCGCCCGACGCTGATCAAGCTCATGCCCGCGCGGATCTCTTCAATGTG 1241
 Db 239 CCGCGGCTCGCGCCCGACGCTGATCAAGCTCATGCCCGCGCGGATCTCTTCAATGTG 298
 QY 1242 CTACGAGGCTCGAAGAAATTAATTTCTGACGAGAAAGAGGAGCGCGGGCGCGGACG 1301
 Db 299 CTACGAGGCTCGAAGAAATTAATTTCTGACGAGAAAGAGGAGCGCGGGCGCGGACG 346
 QY 1302 CCAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGGCGCGCGCCAGAGCTCGAAGCG 1361
 Db 347 CCAGAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGGCGCGCGCCAGAGCTCGAAGCG 406
 QY 1362 TGATCGGCGCATGAACTGATGAAGATTATGTGACCGTCAAAATCAGAAAGAAATGCGT 1421
 Db 407 TGCTCGCCCATGAAACGATGAAGATTATGTGACCGTCAAAATCAGAAAGAAATGCGT 466
 QY 1422 GATTTGAAATTTTGAAGTGAAGGCTTATGGATTTGAATCTTAAGCTGGAAGTGGCG 1481
 Db 467 GATTTGAAATTTTGAAGTGAAGGCTTATGGATTTGAATCTTAAGCTGGAAGTGGCG 525
 QY 1482 CTTAGAAGTTGAATTTGTTTGTTCAGGAAACATGCTCGTTGAGTAATGCCGTCGA 1541
 Db 526 CTTAGAAGTTGAATTTGTTTGTTCAGGAAACATGCTCGTTGAGTAATGCCGTAAT 585
 QY 1542 TGATTTATGCACTTTCTGTATCAATTCATTAAGAAAGATCCACTTTTGAGACC 1598
 Db 586 TGATTTATGCACTTTCTGTG-ATCAATTCATTAAGAAAGATCCACTTTTGAGACC 640

RESULT 5

ADJ42969 standard; cDNA; 661 BP.

ADJ42969;

06-MAY-2004 (first entry)

Plant cDNA #3969.

Plant; gene; ss; transcription; plant genome augmentation; cereal;
 soybean; alfalfa; sunflower; cotton; peanut; tobacco; sugar beet;
 maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 antifungal.

Eukaryota.

US2004016025-A1.

22-JAN-2004.

26-SEP-2002; 2002US-00260238.

26-SEP-2001; 2001US-0325277P.

26-SEP-2001; 2001US-0325448P.

04-APR-2002; 2002US-0370620P.

(BUDWORTH P.
 (MOUGHAMER T.
 (BRIGGS S P.
 (COOPER B.
 (GLAZER)
 GLAZERBROOK J.

PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICHE D.
 PA (ZHU/) ZHU T.
 PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
 PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;
 DR WPI; 2004-190374/18.
 XX
 PT New rice promoter, useful for manipulating crop plants to alter or
 PT improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.
 PS
 PS Example 13; SEQ ID NO 3969; 230bp; English.
 CC The invention relates to plant nucleotide sequences that direct seed-,
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
 CC or constitutive transcription of an operatively linked nucleic acid
 CC segment. The invention also relates to a method for augmenting a plant
 CC genome and a method of identifying a gene, where its expression is
 CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
 CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
 CC encode are useful for manipulating crop plants to alter or improve
 CC phenotypic characteristics, to produce large quantities of oil or
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
 CC have a high nutritional value with reduced apical dominance or dwarfism,
 CC early flowering or altered metabolic pathways. This sequence represents a
 CC plant nucleic acid of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 661 BP; 160 A; 177 C; 202 G; 122 T; 0 U; 0 Other;
 Query Match 31.4%; Score 511; DB 12; Length 661;
 Best Local Similarity 91.7%; Pred. No. 2,3e-88;
 Matches 578; Conservative 0; Mismatches 34; Indels 18; Gaps 3;
 QY 1000 GGCACGTCGCCGACGCTGCTGATCGGCTCGCGCGCGGCCCATAGCCAGCGCCACG 1059
 Db 35 GGCACGTCGCCGACGCTGCTGATCGGCTCGCGCGCGGCCCATAGCCAGCGCCACG 92
 QY 1060 TTCCGCTGAGAGTGGCGCGGAGAGCATGAGTGGGCGCGTGGCGGAGGAGCGAGTG 1119
 Db 93 TTCCGCTGAGAGTGGCGCGGAGAGCATGAGTGGGCGCGTGGCGGAGGAGCGAGTG 152
 QY 1120 TACAAAGACGTCTGCAACGCGATGACTGATCTCTGAGAAAGAGGAGCGCGGGCTC 1179
 Db 153 TACAAAGACGTCTGCAACGCGCATGACTGATCTCTGAGAAAGAGGAGCGCGGGCTC 212
 QY 1180 TACCGCGGCTCGGCGCCGACGTCATCAAGCTCATGCCCGCGCGCATCTTCTCATG 1239
 Db 213 TACCGCGGCTCGGCGCCGACGTCATCAAGCTCATGCCCGCGCGCATCTTCTCATG 272
 QY 1240 TGCTACGAGGCTTGCAAGAAATTAATTTCTGACGAGAAAGAGAGCGCGCGCGGAG 1299
 Db 273 TGCTACGAGGCTTGCAAGAAATTAATTTCTGACGAGAAAGAGAGCGCGCGCGGAG 320
 QY 1300 CCCAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGGCGCGCGCCCAAGAGCTGAGAC 1359
 Db 321 CCCAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGGCGCGCGCCCAAGAGCTGAGAC 380
 QY 1360 GGTGATCGGCGCATGAACTAGATGAAC---ATTATGTGACCGTCAAAATCAGAAAGAA 1415
 Db 381 GGTGATCGGCGCATGAACTAGATGAAGCAAGATTATGTGACCGTCAAAATCAGAAAGAA 440
 QY 1416 ATGCGTGAATTTGAAATTTTGAAGTGTAGAGCTTATGCGATTGAATCTTAAGCTGGAAG 1475

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Db      441 ATGCGTATTTGAATTTTGAAGTTAGAGCCATTCGAATTCCTAGCTGAGAG 500
Qy      1476 TGGGCGCTTGAAGTTGAATTTGTTTGTTCAGGGAAACATGCTCCGTTCACTAATGCC 1535
Db      501 TGGGCGCTTGAAGTTGAATTTGTTTGTTCAGGGAAACATGCTCCGTTCACTAATGCC 560
Qy      1536 GTGGAATGATTTATGACACCTTCTGTATCAATTCATTAAGAAAGTCCACTTTGG 1595
Db      561 GTGGAATGATTTATGACACCTTCTGTATCAATTCATTAAGAAAGTCCACTTTGG 620
Qy      1596 ACCTTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCA 1625
Db      621 ACCTTCAAACTTTGCCCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCA 650

RESULT 6
ADJ42974
ID      ADJ42974 standard; cDNA; 1056 BP.
XX
XX      ADJ42974;
AC
XX      06-MAY-2004 (first entry)
DT
XX
XX      Plant cDNA #3974.
DE
XX
XX      Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.
XX
XX      Eukaryota.
OS
XX
XX      US2004016025-A1.
PN
XX
XX      22-JAN-2004.
PD
XX
XX      26-SEP-2002; 2002US-00260238.
PF
XX
XX      26-SEP-2001; 2001US-0325277P.
PR      26-SEP-2001; 2001US-0325448P.
PR      04-APR-2002; 2002US-0370620P.
XX
XX      (BUDW/) BUDWORTH P.
PA      (MOUN/) MOUNHAMER T.
PA      (BRIG/) BRIGGS S P.
PA      (COOP/) COOPER B.
PA      (GLAZ/) GLAZEBROOK J.
PA      (GOFF/) GOFF S A.
PA      (KATA/) KATAGIRI F.
PA      (KREB/) KREBS J.
PA      (PROV/) PROVART N.
PA      (RICK/) RICHKE D.
PA      (ZHUT/) ZHU T.
XX
XX      Budworth P, Mounhamer T, Briggs SP, Cooper B, Glazebrook J;
PI      Goff SA, Katagiri F, Kreps J, Provart N, Rickse D, Zhu T;
DR      WPI; 2004-190374/18.
XX
XX
XX      New rice promoter, useful for manipulating crop plants to alter or
PT      improve phenotypic characteristics, e.g. produce large quantities of oil
PT      or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT      or high nutritional value.
XX
XX      Example 13; SEQ ID NO 3974; 230pp; English.
XX
XX      The invention relates to plant nucleotide sequences that direct seed-,
CC      leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC      or constitutive transcription of an operatively linked nucleic acid
CC      segment. The invention also relates to a method for augmenting a plant

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CC      genome and a method of identifying a gene, where its expression is
CC      altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC      in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC      canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC      sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC      encode are useful for manipulating crop plants to alter or improve
CC      phenotypic characteristics, to produce large quantities of oil or
CC      proteins, to incur resistance to insecticides, viruses or fungi, and to
CC      incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC      have a high nutritional value with reduced apical dominance or dwarfism,
CC      early flowering or altered metabolic pathways. This sequence represents a
CC      plant nucleic acid of the invention. Note: The sequence data for this
CC      patent did not form part of the printed specification but was obtained in
CC      electronic format directly from USPTO at Seqdata.uspto.gov/Sequence.html.
XX
XX      Sequence 1056 BP; 264 A; 256 C; 288 G; 248 T; 0 U; 0 Other;

Query Match      27.1%; Score 440.4; DB 12; Length 1056;
Best Local Similarity 71.0%; Pred. No. 8.1e-75;
Matches 598; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

Qy      494 CGCCACTGAGAGCATCAGACGACCTGATGTTGGGAGATCCGCGGACTCCATG 553
Db      1 CGCCGTTGAGAGCAATTTAGACACACTGATGGTTGGAGCATGG---GGATTCAATGA 57
Qy      554 CCGGGGTTTTCCGGTGAATCATCGGACGAGGGGTGGCCCGGCTCTTCCGCGCAACG 613
Db      58 CAGAGGTGTTTCAGACAAATATGAGTCGAGGGCTGAGACAGGGCTGTTCCGTTGGAACT 117
Qy      614 CGCTCAACGTCCTCCGCGCTCCGCGGCAAGGCGCATTCAGACCTTCACTTAAGACACG 673
Db      118 TTGTAAATGTTATTCGTTGCTTCCAGCAAGGCGATGAGCTATTTGCTTTGATATAC 177
Qy      674 CGAAGAATGACTGATCCCGCGAGCGGCGAGCGCCAGCAAGTCCCATCCACGCGCG 733
Db      178 CCAAAAATTTCTGACTCCAAAGGCTGATGATGCTCTTAAGACCCCTTCCATCATAC 237
Qy      734 TCGTCCCGGAGGCGCTCGCGGAGTGCCTCAACCTGTGACCTTATCCATGAGCTCG 793
Db      238 TTGTCCGGGGGACATTGACAGGTGTCAAGCTCAACATGACATATCTCTGAACTGA 297
Qy      794 TCAAGACCCGCTCACCATTCAGAAAGAGAGCTGTACACAACTCCCTCCGCGGTGTA 853
Db      298 TCAAGACCCGCTCACCATTCAGAAAGAGAGCTGTATATACAACTTCTCCATGCGCTGTA 357
Qy      854 AGATCGTGGCGAGCAAGAGCGCGGGAGCTGTACCGCGGCTGCGCGCGAGCTGATCG 913
Db      358 AGATTTGACAGAGAGAGGCGCTTCCGAGCTTTTACCGTGTGTGACACGAGCTGATAG 417
Qy      914 GCGTGTGCGGTACCGGCGGCGGCACTTCTAGGCTTACGAGAGCTGCGCGGTGTACC 973
Db      418 GAGTGGTGCAATATGCGCGGACCACTTACGCTTACGACACCTGAGGAGAACTGTACA 477
Qy      974 GCCCGCGGTGGGAGAAAGAGAGTGGGCAAGCTCCGAGAGCTGTGATGGGTCCGCG 1033
Db      478 GGAAGACATTCAGAGAGAGAGATCAGCAACTTGCACCTCTGTATGTTGCGCG 537
Qy      1034 CGGGCGCATAGCCAGACGCGGACGTTCCCGCTGAGAGGTGGCGGAGACAGATGACAG 1093
Db      538 CGGGCGCATCTGAGACCGGCACTTCCCTTCAAGTATGCTCCGACAGCAATGCGAG 597
Qy      1094 TGGGCGCGCTGGGCGGAGGAGAGGTATCAAGAGCTGTGACGCGCATGACTGATCC 1153
Db      598 CAGGGGCGGTGGGCGGAGGAGAGGTATCAAGAGAGGTGTTCCATGCGCTTACTGATTA 657
Qy      1154 TCAGAAAGAGGACCGCGGCTCTACCGCGGCTCGGCGGCTGATGATCAAGTCA 1213
Db      658 TGAGAAAGAGGAGATCGCGGTCTGTACAAAGGGGCTTGGGCCCATGATCAAGTCA 717
Qy      1214 TGGCCGCGCGGCGGACTCTCTCATGTGCTAGAGGCGTGCAGAGAGATCTTGTGACG 1273
Db      718 TGGCCGCGGCGGAGATCTCTGTATGTGCTAGAGGCGTGCAGAGAGATCTTGTGACG 777

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OY      1274  AGAAGAAGACGGCGCGCCCGCGAGCGCCAGAGAGACGAGACCGGACAGCAGGAG 1333
DB      778   CCGAGGAGTGAAGCGAAGTGCAGCCAGGTGTCCGGTCTTTAAAGAAAGGCGCGAGAG 837
OY      1334  GA 1335
DB      838  GA 839

RESULT 7
AAZ20025
ID      AAZ20025 standard, cDNA, 1267 BP.
XX
XX      AAZ20025;
AC
XX      21-DEC-1999 (first entry)
DT
XX
XX      Wheat brittle-1 partial cDNA.
DE
XX      Brittle-1; wheat; carbohydrate; starch; transgenic plant; ss.
XX
XX      Triticum aestivum.
OS
XX
XX      Key      Location/Qualifiers
PH      CDS      2..871
PT      /*tag= a
PT      /partial

PN      MO9949047-A2.
PD
XX      30-SEP-1999.
XX
XX      22-MAR-1999; 99WO-US006583.
XX
XX      26-MAR-1998; 98US-0079420P.
XX
XX      (DUPO ) DU POINT DE NEMOURS & CO E I.
PA
XX
XX      Allen SM, Hiltz WD, Lightner JE, Rafalski JA;
PI
XX      WPI; 1999-591098/50.
DR      P-PSDB; AAY31936.
XX
XX      Novel genes useful in studies of carbohydrate metabolism and function in
PT      plants.
XX
XX      Claim 7; Page 42; 42pp; English.
PS
XX
XX      This nucleotide sequence represents a portion of the cDNA insert in clone
CC      wein, pK0049, ei encoding a portion (see AAY31936) of wheat brittle-1, a
CC      plastidic membrane transporter involved in the transport of ADP-glucose
CC      from the cytosol to the plastid where it is used for starch biosynthesis.
CC      The clone was isolated from a wheat root cDNA library. The invention
CC      relates to isolated nucleic acid fragments (see AAZ20012-25) encoding
CC      plant carbohydrate biosynthetic enzymes (see AAY31923-36) selected from
CC      1,3-beta-D-glucan synthase and brittle-1. It also relates to the
CC      construction of a chimeric gene encoding all or a portion of a
CC      carbohydrate biosynthetic enzyme, in sense or antisense orientation,
CC      where expression of the chimeric gene results in altered levels of
CC      carbohydrate biosynthetic enzyme in a transformed host cell. The
CC      availability of nucleic acids encoding these enzymes will facilitate
CC      studies of carbohydrate metabolism and function in plants, provide
CC      genetic tools for the manipulation of these pathways, and provide a means
XX      to control starch and 1,3-beta-D-glucan biosynthesis in plant cells
XX
XX      Sequence 1267 BP; 351 A; 268 C; 317 G; 331 T; 0 U; 0 Other;
SQ
Query Match      24.6%; Score 400.2; DB 2; Length 1267;
Beat Local Similarity 66.8%; Pred. No. 4,1e-67;
Matches 586; Conservative 0; Mismatches 288; Indels 3; Gaps 1;
OY      415  AGGTCAGATCGGCACCCCGCACTTGGCGCGCTGGTCAGCGGCGCATGCGCGCGCC 474

```

Db	2	AAGATTAAAGTTGGGAATTCACACTCAAGAGGCTCATAGTGGGGGATTTGCAGAGCA	61
Oy	475	GTGTGAGACATTTTCGTGGCGCCACTGAGACGATCAGAGCGCATCTGATGGTGGAGC	534
Db	62	GTGTCAAGGACAGTTGTGGCGCTTTTGGAGACGATTTAGGACACATTTGATGGTCGGCAGC	121
Oy	535	TCGGCGCCGACCTCCATAGCCCGGGGTTTTCCGCTGATCATGCGGACGAGAGGGTGGCC	594
Db	122	AATGGGAATTCATCTACGAGAGGTGTTGAC--TCCATCATGAAGAAATGAGATGCACT	178
Oy	595	GAGCCTTTCCGCGGCAACCGCGTCAAGTCTCTCGCGTCCGCGCCAGCAAGGCCATCGAG	654
Db	179	GAGTTGTTCCGGGCAATTTGGTTAAATGTCATTGAGTCGCGCCGAGCAAGCAATCGAG	238
Oy	655	CACCTTCACTTACGACACGGCGAGAGAGTACTGACCCCGAGGCGCGCGAGCCAGCAAG	714
Db	239	CTTTTGTGCTTTGATACAGCTAAGATTCCTAACCCCAATATGGGGAAGAACAGAG	298
Oy	715	GTCCCATCCCAACGCGCTGTGTGCGGAGCGCTCGCCGAGAGTGGCTACCTGTGC	774
Db	299	ATCCCAATCCCTCTTCACTAGTGGCAGAGGCTTTTCTGTGTCACTCAACTGTGT	358
Oy	775	ACCATCCCAATGAGGCTGTCAACCCGCTCTCCATTCAGAGAGACGTGTAAGCAAC	834
Db	359	ACATACCTCTGGAACCTAATTAACTCGATTTAACCTACAGAGGTGTATGATTAAC	418
Oy	835	CTCCTCCACGCGTTCGTCAAGATCGTGGCGGACGAAAGCCCGGGGAGCTGTACCGCGG	894
Db	419	TTCTCTCATGATTTTGTGAATAATTTGTCCGTGAGAAAGGCCCTGTGAGCTGTATGAGGC	478
Oy	895	CTGGCGCCGAGCCTGATCGGCGTGTGTCGGTACGCGGCGCCAACTTTCACGCTACGAG	954
Db	479	TTAACCCCAAGTCTAATCGAGTGTGTGCATATGACAGCAACCAACTACTTCGCGTATGAC	538
Oy	955	ACGCTGGCGCGCGTGTACCGCGCGCGCATAGCCAGCAGCGGCAAGTTCGCCGAGCG	1014
Db	539	ACCTTTAAGAAAGGTGTCAAGAAATGTTCAAGCAAAATGAATTCGGCAACGTTCCAAAC	598
Oy	1015	CTGCTGATTCGGGATCCGCGCGCGCGCCATAGCCAGCAGCGGCAAGTTCGCCGTGAGAGTG	1074
Db	599	CTGCTCATTTGGGTGTGTGACGAGAGCCATCTCAAGCATCTGCCACATTTCTCTCGAGGTT	658
Oy	1075	GCGCGGAGACAGATGACGTTGGCGCGCGGTGGCGGAGGAGCGAGTGTCAAGAAAGTGTG	1134
Db	659	GCTGCAAGACATAGCAAGTCGAGGCTGTGGCGGCGGGAAGGTATCAAGAACATGCTT	718
Oy	1135	CAGCCCATATATCTGATCTCTCGAGAGAGAGGAGCACGCGCGGCTCTACCGCGGCTCGGC	1194
Db	719	CACGCTCTCTGACCATTTCTCGAGAGAGAAAGGAGGTTGGGGGCGCTTACAGAGGACTGGGG	778
Oy	1195	CCGAGCTGCATCAAGCTCATGCGCGCGCGCGGCATCTCTTCAATGTGCTACGAGAGCTGCG	1254
Db	779	CTTATGTTGCATGAAGCTGTGTGCTGTGCTGTGGGATTTCTGTTTATGTGTCTAGAACTTGC	838
Oy	1255	AAGAAATACTTGTTCAGACGAGAAAGAAAGACGCGCGCG	1291
Db	839	AAGAAATACTGATTTGAGAGAAAGAAAGATGAAGCG	875
RESULT 8			
AAD57636			
AAD57636 standard; DNA; 1140 BP.			
XX	AAD57636;		
AC			
XX	20-NOV-2003 (first entry)		
DT			
XX			
DE	Rice grain quality and nutritional composition gene, BTL.		
XX			
KM	Rice; abiotic stress tolerance; pathogen resistance; disease resistance;		
XX	grain quality; nutritional content; plant yield; BTL; plant; gene; de.		
OS	Oryza sativa.		

XX Key Location/Qualifiers
 FH CDS 1.1140
 FT /*tag= a
 FT /product= "Rice Bt1 protein"
 PN WO2003048319-A2.
 XX
 PD 12-JUN-2003.
 PF 27-NOV-2002; 2002WO-US038359.
 XX
 PR 30-NOV-2001; 2001US-0334501P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Sainz MB, Salmeron J, Weislo L;
 XX
 DR WPI; 2003-505288/47.
 XX
 DR P-PSDB; AAE38268.
 XX
 PT New nucleic acid from *Oryza sativa*, useful for altering abiotic stresses
 PT tolerance, pathogen or disease resistance or the grain quality,
 PT nutritional content or yield in a plant.
 XX
 PS Claim 2; Page 144-145; 223pp; English.
 XX
 CC The invention relates to nucleic acid molecules from rice encoding
 CC proteins for abiotic stress tolerance, enhanced pathogen or disease
 CC resistance and altered nutritional quality. The sequences of the
 CC invention are useful for altering abiotic stress tolerance, pathogen or
 CC disease resistance or the grain quality, nutritional content or yield in
 CC a plant. The present sequence is rice grain quality and nutritional
 CC composition gene, Bt1
 XX
 SQ Sequence 1140 BP; 277 A; 283 C; 318 G; 262 T; 0 U; 0 Other;
 Query Match 24.5%; Score 397.6; DB 10; Length 1140;
 Best Local Similarity 70.2%; Pred. No. 1.3e-66;
 Matches 563; Conservative 0; Mismatches 234; Indels 5; Gaps 2;

QY 362 AGGCCCAAGAGCGCAAAAGGCGCAAGAGCTGATCTGAGAGAGGTGAGGTCA 421
 DB 344 AGGTGTGTGATGCAAGAGCTGTGAAGAAAGCAAGAAAGCTGAGCTGAAGCTGAATTA 403
 QY 422 AGATCGCAACCCGCACTGCGCGCTGTGTCAACCGCGCCATGCGCGCGCTGTGCA 481
 DB 404 AGATTGGGAACCCCATTTGAGCGCTGTGTAGCGGAGCGGTTGCGGAGCTGTGCA 463
 QY 482 GGAATTTGTGTGCGCACTGAGAGAGATCAAGAGCACTGATGTGAGGAGCTCCGCG 541
 DB 464 GGAATTTGTGTGCGCACTGAGAGAGATCAAGAGCACTGATGTGAGGAGCTCCGCG 521
 QY 542 CCGAATTCATGCGCGGAGTTTCCGATGATGCGAGCGAGGAGTGGCCCGCTCT 601
 DB 522 -GAGCTGTATGACAGAGGATTTCCAGTCAATCAAGAGCGAGGAGTGGAGCAAGCTGT 580
 QY 602 TCGCGGCAACCGCTCAACGTCTCCGCGTGGCGCCAGAGAGCCATGAGCACTTCA 661
 DB 581 TCCGTGGGAACCTTTGTCAATGTCAATCGAGTTGACCAAGAGCAATTAAGTATTGG 640
 QY 662 CTTAGCAAGCGGAGAGAGTGAACCTGAGCCCGAGCGCGGAGCCAGCCAAAGTCCGCA 721
 DB 641 CTTTCGATACAGCCAGAAATTTCTTAATCCAAAGGCTGATGATGCCCTTAAGACACCT 700
 QY 722 TCCCAAGCGCGCTGTGCGCGAGCGCTGCGCGAGTGGCGCTCAACCTGTGACCTATC 781
 DB 701 TCCCTCATGCTTATTGTGTGAGCACTGTGCGGTTAGCTCAACATTTGACATAC 760
 QY 782 CCATGAGAGCTGTCAAGAGCCGCTCACCATGAGAGAGAGAGTGTAGCAACCTCTCC 841
 DB 761 CTTTGAATGATCAAGAGCCGATTTGACTATTGAGAAAGATGTCTATTAACAATCTCTCC 820

QY 842 ACGCTTTCGATAGATCTGTGCGGACGAAAGCCCGGAGAGCTGTACCGCGGCTGCGC 901
 DB 821 ATGCTTTCGATCAAGATCTACGAGAGAGAGCC--CTCAGCTCTACCGGCTTACAC 878
 QY 902 CGAGCTTGTTCGCGCGTGTGCGCTGACGCGCGCACTTCTACGCTTACGAGCGTGC 961
 DB 879 CGAGTGTGATCGCGCGTGTGCGCTGACGCGCAATTAATGTGCTTACGAGACCTTGA 938
 QY 962 GCGCGTGTACCGCGCGCTGCGGAGAAAGAGAGTGGGCAACGTCCGACGCTGCTGA 1021
 DB 939 AGAAGCTCTACGAGAGACATTCACAGAGAGAGATCAAGACATCGGAGCTTCTCA 998
 QY 1022 TCGGATTCGCGCGCGCGCCATACGACACGCGCACTTCCCGCTGAGAGTGGCGCGA 1081
 DB 999 TCGGTTCAAGCGCGGCGTGCATCTCGAGCACCGCCACTTCCCTCTCGAGTGTCTGCA 1058
 QY 1082 AGCAGATGCAAGTGTGCGCGCTGTGCGGAGAGAGAGTGTACAAAGAGTGTCAAGCCA 1141
 DB 1059 AGCAATGCAAGTGTGAGCGGTAGCGCGAGCGAGGTCTACAAAGATGTCTTCAATGCTC 1118
 QY 1142 TGTACTGATCTCTCGAGAAAGA 1163
 DB 1119 TGTATTGATTAATGAGAAATGA 1140

RESULT 9
 AAZ20024
 ID AAZ20024 standard; cDNA; 449 BP.
 XX
 AC AAZ20024;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Wheat brittle-1 partial cDNA.
 XX
 KW Brittle-1; wheat; carbohydrate; starch; transgenic plant; ss.
 XX
 OS Triticum aestivum.
 XX
 FH Key Location/Qualifiers
 FT CDS 74.400
 FT /*tag= a
 FT /partial
 PN WO949047-A2.
 PD 30-SEP-1999.
 XX
 PF 22-MAR-1999; 99WO-US006583.
 XX
 PR 26-MAR-1998; 98US-0079420P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Allen SM, Hitz WD, Lightner JF, Rafalski JA;
 XX
 DR WPI; 1999-591098/50.
 XX
 DR P-PSDB; AAY31935.
 PT Novel genes useful in studies of carbohydrate metabolism and function in
 PT plants.
 XX
 PS Claim 7; Page 41; 42pp; English.
 XX
 CC This nucleotide sequence represents a portion of the cDNA insert in clone
 CC wdk1c.pK012.c23 encoding a portion (see AAY31935) of wheat brittle-1, a
 CC plastidic membrane transporter involved in the transport of ADP-glucose
 CC from the cytosol to the plastid where it is used for starch biosynthesis.
 CC The clone was isolated from a wheat kernel cDNA library. The invention
 CC relates to isolated nucleic acid fragments (see AAZ20012-25) encoding
 CC plant carbohydrate biosynthetic enzymes (see AAY31923-36) selected from
 CC 1,3-Beta-D-glucan synthase and brittle-1. It also relates to a
 CC construction of a chimeric gene encoding all or a portion of a

CC carboxylate biosynthetic enzyme in sense or antisense orientation,
CC where expression of the chimeric gene results in altered levels of
CC carboxylate biosynthetic enzyme in a transformed host cell. The
CC availability of nucleic acids encoding these enzymes will facilitate
CC studies of carboxylate metabolism and function in plants, provide
CC genetic tools for the manipulation of these pathways, and provide a means
CC to control starch and 1,3-beta-D-Glucan biosynthesis in plant cells
XQ
Sequence 449 BP; 97 A; 134 C; 149 G; 65 T; 0 U; 4 Other;

Query Match	24.2%	Score 392.6	DB 2	Length 449
Best Local Similarity	96.4%	Pred. NO. 1e-65		
Matches 432; Conservative	0	Mismatches 12	Indels 4	Gaps 3

Qy	1	GGCCAGTAGGAGGTGAAGGACTGTAAGAACTCTAGGCGAGGGCCAGTATCAGTTCTGTCT	60
Db	1	GGCCANTGAGGGAGGTGAAGGACTGTAAGAACTCTTAGGCGAGGGCAGCTATCAGTTCTGTCT	60
Qy	61	TGCTTCTCTCG--AGATGGCGGGCGGCAATGGCCGCGAGAGCAATGTGTACCAAGAACAAACCG	119
Db	61	TGCTTCTCTGGAAGATGGCGGGCGGCAATGGCCGCGAGAGCAATGTGTACCAAGAACAAACCG	120
Qy	120	CGCCTCGCTCGTCATGAGCAAGAAAGAACTGTATTATGGCGGCGGTCCCTGAGGTGCGCTT	179
Db	121	CGCCTCGCTCGTCATGAGCAAGAAAGAACTGTATTATGGCGGCGGTCCCTGAGGTGCGCTT	180
Qy	180	CCCTTTGAGACTGGCAGCCCGGAGTCCAGAGACTTTGACTTCCACGCAAGGCTCTGTTCCG	239
Db	181	CCCTTTGAGACTGGCAGCCCGGAGTCCAGAGACTTTGACTTCCACGCAAGGCTCTGTTCCG	240
Qy	240	CAGCGTGGAGACTCAGACCTGTGCCAGCGGCCGCCGCGGTAGCGCGGAGACTATGACGGAA	299
Db	241	CAGCGTGGAGACTCAGACCTGTGCCAGCGGCCGCCGCGGTAGCGCGGAGACTATGACGGAA	300
Qy	300	GGCTTGGGCCCGCCGACGAGCTGGCACACC--AGCTGGCAAGCCGGCGGGCGAGGCGGGCTGCC	358
Db	301	GGCTTGGGCCCGCCGACGAGCTGGCACACCAGCAACCTGGCAATCCGCGGGCGAGGCGGGCTGCC	360
Qy	359	AGAAAGCCCAAGAGCGCAAAAAAGCGCAAAAAACAGAGCTGAGTGTGA--GGAAAGGTGAG	416
Db	361	AGAAAGCCCAAGAGCGCAAAAAAGCGCAAAAAACAGAGCTGAGTGTGAAGGTGAG	420
Qy	417	GGTCAAGATGGCAACCCGCACTCTGGG	444
Db	421	GGTCAAGATGGCAACCCGCACTCTGGG	448

RESULT 10
ADJ42975
ID ADJ42975 standard; cDNA; 1099 BP.

XX		
AC	ABD42975;	
XX		
DT	06-MAY-2004	(first entry)
XX		
DE	Plant cDNA #3975.	
XX		
KW	Plant; gene; ss; transcription; plant genome augmentation; cereal;	
KW	soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;	
KW	maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;	
KW	stress tolerance; salt tolerance; cold tolerance; drought tolerance;	
KW	plant nutrition; apical dominance; dwarfism; early flowering; antiviral;	
XX	antifungal.	
XX		
OS	Eukaryota.	
XX		
XX		
PN	US2004016025-A1.	
XX		
PD	22-JAN-2004.	
XX		
EP	26-SEP-2002; 2002US-00260238.	
XX		
PR	26-SEP-2001; 2001US-0325277P.	

PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.

XX
PA (BUDM//) BUDNORTH P.
PA (MOUG//) MOUGHAMER T.
PA (ARIG//) BRIGGS S P.
PA (COOP//) COOPER B.
PA (GLAZ//) GLAZEBROOK J.
PA (GOFF//) GOLF S A.
PA (KATA//) KATAGIRI F.
PA (KREP//) KREPS J.
PA (PROV//) PROVART N.
PA (RICK//) RICKS D.
PA (ZHUT//) ZHU T.

PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J
PI Goff SA, Katagiri F, Keps J, Provant N, Ricke D, Zhu T;
XX
DR WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.

PS Example 13; SEQ ID NO 3975; 230bp; English.

CC The invention relates to plant nucleotide sequences that direct seed-
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g., soybean, alfalfa, sunflower,
CC cornola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g., salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
XX

Sequence 1099 BP; 277 A; 254 C; 286 G; 282 T; 0 U; 0 Other;

Sequence	1099	BP	277	A	254	C	286	G	282	T	0	U	0	Other
Query Match	22.3%	Score	361.6	DB	12	Length	1059							
Best Local Similarity	72.7%	Pred. No.	9	9e-60										
Matches	481	Conservative	0	Mismatches	179	Indels	2	Gaps	1					

<i>Oy</i>	631	GTGGCGGCAAGCAAGGCATCGACACTTCACTTAACGACAGGGCGAAGAATACCTGACC	690
<i>Dh</i>	1	GTTTGCTCAAAGCAAGGGGATTGAGCTTAGTTCCTT--GATACAGCCAAAATAATCCTGACT	58
<i>Oy</i>	691	CCGGAGGCCGGCGAGCCAGCCAAGATGCCCATCCCAAGCCGCGCTGTGCGCCGAGGCGCTC	750
<i>Dh</i>	59	CCAAAGGCTATGATCTCTCTAABAAGTCCCTTTCCTCATCACTGTGGCGGGGGGGAAGTT	118
<i>Oy</i>	751	GCCGAGTGGCGGTCAACCTGTGCACTATCCATGAGGCTGTGAAGACCCGCTCACCC	810
<i>Dh</i>	119	GCAGGTCTCAGCTCAACAAGCTGCAATATCCTCTGGAATCGATCAAGAACCCGCTGAAT	178
<i>Oy</i>	811	ATGSAAGAAGACGATGACGAACAAGCTCCTCCACAGGTTCCGACAAATGCTGGCGACGAA	870
<i>Dh</i>	179	ATAGAGAAAGATGTATATGACAAGCTTCTCAATTGCTCTGTCAAGATTGTAGAGAGGAA	238
<i>Oy</i>	871	GGCCCGGGGAGAGCTATACCGCGGCGTGGCGCCGAGCTGATCGGCGTGTGCTCTAAGCG	930
<i>Dh</i>	239	GGCCCCCTCGAGAGCTTACCGTGTCTACACCGGAGTCTGATAGAGATGTGTCCATACGCC	298
<i>Oy</i>	931	GCGGCAACTTCTAAGCCTACGAGACGCTGCGGCGGTGTAACCGCGCGCGCTCGGGGAAA	990

QY	633	GTGCGGCCAAGAAAGGCATGAGGACTTCATCTTACGACAGGGGAAAGAAAGTACTACG	690
Db	1	GTGTCTCCAGAGAGGCGATTGAGTATTGCTTT--GATACGCCAAAAATTCCTGACT	58
QY	691	CCGAGAGCCCGGAGCCAGCCAAAGGTCCCATCCCAAGCCGCTGTTGCGAGAGCGCTC	750
Db	59	CCAAAGGCTGATGATATCTCTTAAGACTCCCTTTCTCCTCATCACTGTGTGCGGGGCACTT	118
QY	751	GGCCGAGTGGGCTCAACCTGTGACCTATCCATGTAGAGCTGTCAGAGCCCGTCTACC	810
QY	119	GCAAGGTGAGCTCAACACTTGCACATATCTCTGAACTGATCAGAACCCGTTGACT	178
QY	811	ATCGAAGAGAGCTGTACGACAACTCCTCCAGCGGTTGTCAGAGATCTGCGCGACGAA	870
Db	179	ATVAGAAAGATGATATAGACAACTTCTCAATTGCGCTCGTCAAGATTGTATACGAGAGAA	238
QY	871	GGCGCGGGGAGACTGTACCGGGGCTGGCGCGCGAGCGTGATCGGCGGTGGTCGCTAGCG	930
Db	239	GGCGCCCTCGAGACTTTACCGTGGTGTGACACCGAGTCTGATAGAGTGGTGTCCATAGCC	298
QY	931	GGGCGCAATTTTACGCTTACGAGAGCGTGGCGGCGGTGATACGCGCGCGGTTCGGGAAA	990

Db 299 GCACCAACTACTATGCTTACGACACCTGAGGAGAGCTTACAGAGATTCAGACAG 358
QY 991 GAGAGGTGGGCAACGCGCCGACGCTGCTGATGCGGCTCCGCGCGGCGGCATAGCCAGC 1050
Db 359 GAGAGATTCAGCAACATTGCAACTCTCTGATCGGCTCGCGCGGCGGCATCTCGAGC 418
QY 1051 ACGGCGCATCTTCCCGCTGAGTGCGCGGAGAGATGAGAGGTGGCGCGCTGCGCGG 1110
Db 419 ACGGCGCATCTTCCCGCTGAGTGCGCGGAGAGATGAGAGGTGGCGCGCTGCGCGG 478
QY 1111 AGCGAGGTGTCAGAGAAAGTGTGTCAGCGCCATGTACTGTCACTCTCCGAGAGAGGCGCAC 1170
Db 479 AGCGAGGTGTCAGAGAAAGTGTGTCAGCGCTCTACTGTCACTATGAGAGAGAGGCGATC 538
QY 1171 GCGGCGCTTACCGCGCGGCTCGCGCCGAGCTGATCAAGCTCATGCCGCGCGCGCATC 1230
Db 539 GCGGCGCTTACAGAGGCGCTTGGCGCTGATCAAGCTCATGCCGCGCGCGGATC 598
QY 1231 TCCTTCATGTGCTACGAGCGCTGCAAGAGATCTTGTGACGAGAGAGACGCGCGC 1290
Db 599 TCCTTCATGTGCTACGAGCGCTGCAAGAGATCTGCTCGAAGCGGAGTGAACGAA 658
QY 1291 GC 1292
Db 659 GC 660

RESULT 11

AAC49806
ID AAC49806 standard; DNA; 1331 BP.

XX AAC49806;
XX

DT 18-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62505.
XX

KM Hybridisation assay; Genetic mapping; Gene expression control;
XX

KW protein identification; signal transduction pathway; metabolic pathway;
XX

OS Arabidopsis thaliana.
XX

PN EPI033405-A2.
XX

PD 06-SEP-2000.
XX

XX 25-FEB-2000; 2000EP-00301439.
PF

XX 25-FEB-1999; 99US-0121825P.
PR

PR 05-MAR-1999; 99US-0123180P.
PR

PR 09-MAR-1999; 99US-0123548P.
PR

PR 23-MAR-1999; 99US-0125788P.
PR

PR 25-MAR-1999; 99US-0126264P.
PR

PR 29-MAR-1999; 99US-0126785P.
PR

PR 01-APR-1999; 99US-0127462P.
PR

PR 06-APR-1999; 99US-0128234P.
PR

PR 08-APR-1999; 99US-0128714P.
PR

PR 16-APR-1999; 99US-0129845P.
PR

PR 19-APR-1999; 99US-0130077P.
PR

PR 21-APR-1999; 99US-0130449P.
PR

PR 23-APR-1999; 99US-0130510P.
PR

PR 28-APR-1999; 99US-0130891P.
PR

PR 30-APR-1999; 99US-0131449P.
PR

PR 30-APR-1999; 99US-0132048P.
PR

PR 04-MAY-1999; 99US-0132407P.
PR

PR 05-MAY-1999; 99US-0132484P.
PR

PR 06-MAY-1999; 99US-0132485P.
PR

PR 06-MAY-1999; 99US-0132486P.
PR

PR 07-MAY-1999; 99US-0132487P.
PR

PR 11-MAY-1999; 99US-0132863P.
PR

PR 11-MAY-1999; 99US-0134256P.
PR

PR 14-MAY-1999; 99US-0134218P.
PR

PR 14-MAY-1999; 99US-0134219P.
PR

PR 14-MAY-1999; 99US-0134221P.
PR

PR 14-MAY-1999; 99US-0134370P.
PR

PR 18-MAY-1999; 99US-0134788P.
PR

PR 19-MAY-1999; 99US-0134941P.
PR

PR 20-MAY-1999; 99US-0135124P.
PR

PR 21-MAY-1999; 99US-0135353P.
PR

PR 24-MAY-1999; 99US-0135629P.
PR

PR 25-MAY-1999; 99US-0136021P.
PR

PR 27-MAY-1999; 99US-0136392P.
PR

PR 28-MAY-1999; 99US-0136782P.
PR

PR 01-JUN-1999; 99US-0137222P.
PR

PR 03-JUN-1999; 99US-0137528P.
PR

PR 04-JUN-1999; 99US-0137502P.
PR

PR 07-JUN-1999; 99US-0137724P.
PR

PR 08-JUN-1999; 99US-0138094P.
PR

PR 10-JUN-1999; 99US-0138540P.
PR

PR 10-JUN-1999; 99US-0138847P.
PR

PR 14-JUN-1999; 99US-0139119P.
PR

PR 16-JUN-1999; 99US-0139452P.
PR

PR 16-JUN-1999; 99US-0139453P.
PR

PR 17-JUN-1999; 99US-0139492P.
PR

PR 18-JUN-1999; 99US-0139454P.
PR

PR 18-JUN-1999; 99US-0139455P.
PR

PR 18-JUN-1999; 99US-0139456P.
PR

PR 18-JUN-1999; 99US-0139457P.
PR

PR 18-JUN-1999; 99US-0139458P.
PR

PR 18-JUN-1999; 99US-0139459P.
PR

PR 18-JUN-1999; 99US-0139460P.
PR

PR 18-JUN-1999; 99US-0139461P.
PR

PR 18-JUN-1999; 99US-0139462P.
PR

PR 18-JUN-1999; 99US-0139463P.
PR

PR 18-JUN-1999; 99US-0139750P.
PR

PR 18-JUN-1999; 99US-0139763P.
PR

PR 21-JUN-1999; 99US-0139817P.
PR

PR 22-JUN-1999; 99US-0139899P.
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PR 23-JUN-1999; 99US-0140353P.
PR

PR 23-JUN-1999; 99US-0140354P.
PR

PR 24-JUN-1999; 99US-0140695P.
PR

PR 26-JUN-1999; 99US-0140823P.
PR

PR 29-JUN-1999; 99US-0140991P.
PR

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KW      Hybridisation assay; genetic mapping; gene expression control;
KM      protein identification; signal transduction pathway; metabolic pathway;
KW      promoter; termination sequence; ss.
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DB 471 TAAATGATGGAGG---TGAGAGAACTCCAGACTGAACTGTTCATGATATCATTAAGC 527
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RESULT 13
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AC 06-MAY-2004 (first entry)
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KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;

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Db 125 TGACATACCTCTTGAAGTCAAGACTGCTTACCAATTCAAGAGGTGTTTCAAG 184
QY 833 ACCTCTCCACGCGCTTGTGTCAGATCGTGCAGACGAGCCGCGGAGCTGTACCGCG 892
Db 185 GGATTTTGTAGTGCCTTTCTCAAAATCATACCGGAGAAAGACCAACAGACTCTACAGG 244
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
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DB 65 AATCCCAATTCAGCTTCTTACTGCTGGTGTGCTGAGTTAGCCAGACATCT 124
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-659-199-17

Perfect score: 1625
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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12: gb sy: *
13: gb un: *
14: gb vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	735.8	45.3	1662	8 AK107368	AK107368 Oryza sat
5	723.2	44.5	927	8 AY033629	Hordeum v
6	666	41.0	1733	8 MZEBT1A	M79333 Zea mays br
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ALIGNMENTS

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ACCESSION	AR438061	Sequence 17 from patent US 6660850.	1625 bp	DNA	linear	PAT 18-DEC-2003
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KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1625)					
AUTHORS	Allen,S.M., Lightner,J.E. and Rafaleki,J.A.					
TITLE	Nucleic acid encoding a wheat brittle-1 homolog					
JOURNAL	Patent: US 6660850-A 17 09-DEC-2003;					
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RESULT 2
BT008958
LOCUS Triticum aestivum clone wdk1c.pk012.c23.file, full insert mRNA
DEFINITION
ACCESSION BT008958
VERSION BT008958.1 GI:32128509
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 1625)
Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
Direct Submission
Submitted (20-JUN-2003) Crop Genetics, B. I. Dupont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA

FEATURES
source
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3,7e-217;
Matches 1625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1561 GTATCAATTCATTAAG 1620
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 Db 1621 AAAAA 1625

RESULT 3
 AY560327
 LOCUS
 DEFINITION
 Hordeum vulgare subsp. vulgare plastidial ADP-glucose transporter
 mRNA, complete cds; nuclear gene for plastid product.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 1191)
 Patron, N.J., Greber, B., Fahy, B.F., Laurie, D.A., Parker, M.L. and
 Denyer, K.

TITLE
 The 1191 Mutations of Barley Reveal the Nature and Importance of
 Plastidial ADP-Glc Transporters for Starch Synthesis in Cereal
 Endosperm
 JOURNAL
 PLANT PHYSIOL. 135 (4), 2088-2097 (2004)
 PUBMED
 15299120
 REFERENCE
 2 (bases 1 to 1191)
 Patron, N.J.

TITLE
 Direct Submission
 Submitted (26-FEB-2004) Metabolic Biology, John Innes Centre,
 Colney Lane, Norwich, Norfolk NR4 7UH, UK
 JOURNAL
 Location/Qualifiers

FEATURES
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 GVASLTCTYPMELVKTLLTEKDYVLDLHAFVIVADEGGEGLYRGLAPBLIGVVPY
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ORIGIN
 Query Match 65.8%; Score 1069; DB 8; Length 1191;
 Best Local Similarity 93.7%; Pred. No. 1.2e-119;
 Matches 1136; Conservative 0; Mismatches 50; Indels 27; Gaps 1;

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Db 181 AGCTGTCCCAAC-----GACGGGAAGGCTCGCGCGCGC 213
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RESULT 4
AKI07368
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:002-127-B01, full
insert sequence.
ACCESSION
AKI07368
VERSION
AKI07368.1 GI:3292577
KEYWORDS
FLI cDNA; oligo capping.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioidae; Oryzaceae; Oryza.
REFERENCE
1
The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Oono, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Maeda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishida, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Komoto, H., Miyazaki, A., Oono, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
JOURNAL
MEDLINE
PUBMED
22752273
12869764
2 (bases 1 to 1662)
REFERENCE
AUTHORS
Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashidume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hironaka, K., Hirooka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
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Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, R., Nishida, J., Nishi, K., Nomura, K.,
Nunakata, R., Ohneda, E., Oono, M., Ohtsuki, K., Oka, M., Ooka, H.,
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Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
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Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.
TITLE
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of

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ORIGIN

Query Match 41.0%; Score 666; DB 8; Length 1733;
Best Local Similarity 80.2%; Pred. No. 1.8e-83;
Matches 810; Conservative 0; Mismatches 190; Indels 10; Gaps 2;

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362 AGCGCCAGAGCGAG 421
413 GCGGCGGCGAG 472
422 AGATCGGCAACCGGACCTGCGCGCGCGCTGCTGACGCGCGCGCGCGCGCGCGCGCTGCTGA 481
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542 CGGACTCCATGAGCG 601
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Db 1072 CGCTGCTATCGGCG 1131
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RESULT 7
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:J033130A21, full insert sequence.
ACCESSION
AK103471
VERSION
AK103471.1 GI:32988680
KEYWORDS
FLI CDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
1
The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team., Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Oono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikiura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Osaio, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
TITLE
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL
Science 301 (5631), 376-379 (2003)
MEDLINE
22752273
PUBMED
12869764
2 (bases 1 to 1968)
REFERENCES
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, J., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,

Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariikawa, R., Nikiura, J., Nihi, K., Nomura, K., Numaaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cdna/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Shikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PLS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Iehibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hamagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiyamato, K., Hiroaka, D., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numaaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES
Source Location/Qualifiers

1..1968
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiyar="Nipponbare"
/db_xref="taxon:39947"
/clone="U033130A21"

ORIGIN

Query Match 26.8%; Score 435; DB 8; Length 1968;
Best Local Similarity 66.2%; Pred. No. 2.8e-51;
Matches 643; Conservative 0; Mismatches 325; Indels 3; Gaps 1;

DY 316 GACGTGCACACGACGTCGAGCCGCGGAGCGGCGCTCCAGAAAGCCAGAAAGCG 375
Db 647 GAGATCGAGCACATGCTCTGCCGCGTCAAGTGTGAGGTGAGCTAATGAGAAAGGG 706

DY 376 AAAAAGCCAAAAGCGACGCTGAGTCTAGAGAGGTGAGGTCAAGATCGGCAACCG 435
Db 707 AAGAGAAAGAAAGAAAGAAAGAAATTAAGCAATTCAGATCAAGATCAAGAGTGGCGAAATCC 766

DY 436 CACCTGGCGGCGCTGCTGACGAGCGCGCGCGCGCGCGCTGTCAGAGACTTTGTCGGC 495
Db 767 CACCTGAAGAGGCTGATCAAGCGGCGGAGATGCGCGCGGCTGTGAGAGAGCGCGCTGCG 826

DY 496 CCACTGGAGAGATCAAGAGCGCACTGATGATGGGAGCTCCGCGCGCGCATCGGCC 555

Db 827 CCAATTGAGACGATCAAGCGACGCACTTTGATGATGGGAGTAATGG--GAATTGACCGCG 883
DY 556 GGGGTTTTCCGGTGTGATCATGCGAGCGAGGGGTGGCCCGGCTCTTCGCGCGCAAGCG 615
Db 884 GAGGTTCACATGTCATCATGAGCATGAGAGGTGACGTGGTGTTCGGCGTAATCTT 943
DY 616 GTCAACGTCCTCCGCTGCGCGCCAGCAAGCCATCGAGCACTTCACTTAACGACCGCG 675
Db 944 GTTAATGATTCATGATCGATCGCCCGCGCAAGCAATTAAGACTCTTCCTTTGATACAGCT 1003
DY 676 AAGAAATACCTGACCCCGGAGCGCGCGAGCCAGCCAAAGTCCCATCCCAAGCGCGCTC 735
Db 1004 AACCAATTTCTTGAACCCCAATCTGGGAGCAAAAGAAAGATCCCACTCCCTTACATA 1063
DY 736 GTCCGCGAGCGCTGCGCGGAGTGGCGTCAACCTGTGACCTATCCATGAGCTGCTC 795
Db 1064 GTGGCTGGGAGCATTTCTGTGTGATGATTAACCTCTGTATCTTACCTTGAAATTAAT 1123
DY 796 AAGACCCGTCCTCACATCGAAGAGAGCGTGAACGACAACTCTCCAGCGCTTCGTAAG 855
Db 1124 AAGACACAGTTAATCAATACAGAGAGGTATATGATTAATTTCTCACCGCTTGTCAAA 1183
DY 856 ATGTCGCGAG 915
Db 1184 ATGTCCGTGAAG 1243
DY 916 GTGTCGCGAG 975
Db 1244 GTTGTCCATATGCGCGAG 1303
DY 976 CGGCGTCGCGGAG 1035
Db 1304 AAGATGTCAG 1363
DY 1036 GGGGCGATAGCAG 1095
Db 1364 GGGGCTATTCAG 1423
DY 1096 GGGGCGGTGGGAG 1155
Db 1424 GGGCGAGTGTGAG 1483
DY 1156 GAG 1215
Db 1484 GAGGATGAAG 1543
DY 1216 CCGCGCGCGGAGATCTCTTCATGTGCTACAGAGCTTCGAAGAGATCTTGTCCAGAG 1275
Db 1544 CCAGCGCGCGGATTTTCGTTATGTGCTATGAGGCTTGAAGAGAGATTTGAACAAGAGAA 1603
DY 1276 AAGAGAGAGAG 1286
Db 1604 GAGGATGACTG 1614

RESULT 8
AR438062 1267 bp DNA linear PART 18-DEC-2003

LOCUS AR438062 Sequence 19 from patent US 6660850.
DEFINITION AR438062
ACCESSION AR438062
VERSION AR438062.1 GI:40204513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1267)

AUTHORS Allen, S.M., Lightner, J.B. and Rafalski, J.A.
TITLE Nucleic acid encoding a wheat brittle-1 homolog
JOURNAL Patent: US 6660850-A 19 09-DEC-2003;
FEATURES Location/Qualifiers
1..1267
/organism="unknown"

ORIGIN /mol_type="genomic DNA"

Query Match 24.6%; Score 400.2; DB 6; Length 1267;
Best Local Similarity 66.8%; Pred. No. 2.1e-46;
Matches 586; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

QY 415 AGGCTCAAGATCGGCAACCGCACTGCGCGCGCTGTGAGCGGCGCCATCGCGCGCGC 474
DB 2 AAGATTAAAGTTCGGAAATTCACCTCAAGAGGCTCATCATGTGGGGGATTGACAGCA 61
QY 475 GTGTGAGAGACTTTCGTGCGCGCACTGAGACGATCAGACGCACTGATGTGGGAGC 534
DB 62 GTGTCAAGACAGTTGTGGCGCTTTGAGAGCAATTAGACACATTTATGTGGCGCAGC 121
QY 535 TCCGCGCGCGACTCCATGCGCGCGGCTTTCCGCTGATCATGCGAGCGAGGGGTGCC 594
DB 122 AATGGGAATTCATCTACGAGAGGTGTTGAC---TCCATCATGAAAGATGAGATGACT 178
QY 595 GGCCTCTTCGCGCGCAACCGCGCTCAAGCTCTCCGCGCGCGCAAGGCGCATCGAG 654
DB 179 GGGTGTTCGCGCGCAATTTGGTTATGTCAATTCAGTGCCTCCGCGCAAGCAATCGAG 238
QY 655 CACTTCACCTTACGACACGCGCGAAGATCTGACCCCGAGGCGCGCGAGCCAGCCAG 714
DB 239 CTTTTCCTTTGATGATACGCTAAGAGTTCCTAACCCCAATCTGGGGAAGACAGAG 298
QY 715 GTTCCCATCCCAACCGCGCTGTCGCGAGCGCTGCGGAGTGCGCTCAACCTGTGTC 774
DB 299 ATCCCAATCCCTTCCTTCACTAGTGGGAGGCTTTTGTGTGTCAGCTCAACTGCTGT 358
QY 775 ACCCTATCCCATGAGAGTGTCTCAAGACCGCTCTCACATGAGAGAGAGTGTACAGAC 834
DB 359 ACATACCTCTGGAACCTAATTAAGACTCATTAACCATACAGAGGTGTATGATTAAC 418
QY 835 CTCCTCAACGCGCTTCGTCAGATCTGTCGCGAGAGGCGCGGAGCTGTACCGCGAG 894
DB 419 TTCCTCAATGCTTTGTGAAATTTGTCGTGAAGAGGCGCTGTGAGCTGTATGAGGC 478
QY 895 CTGGGCGCGAGCTGATGCGCGCTGTGTCGCTGACGCGCGCGCACTTCTACCGCTAC 954
DB 479 TTAAACCCCAAGCTATCGAGTGTGTCATATGACAGCAACCACTTCCGCTATGAC 538
QY 955 AGCGTGGCGGAGTGTACCGCGCGCTGTGGGGAAGAGAGTGTGGGGAACCTTCCGAG 1014
DB 539 ACCCTTAAGAGGTGTACAAAGAAATGTTCAAGACCAATGGAATGCGCAACGTTCCA 598
QY 1015 CTGCTGATCGGGTTCGCGCGCGCGCGCATAGCCAGACGCGCAACGTTCCGCTGAG 1074
DB 599 CTGCTCATTTGGGTCTGTGCGAGAGGCTCATAGCATCTGCTCAATTTCTCTCAAG 658
QY 1075 GCGCGGAGACAGATGAGGTGGGCGCGCTGTGGGCGGAGGAGGTGTACAGAACGTG 1134
DB 659 GCTCCCAAGCATGTGAGTGTGAGGCTGTGGCGCGCGAGGTATACAAAGACATGCTT 718
QY 1135 CACGCGATGTACTGATCTCTCGAAGAGAGGCAACCGCGGCTCTACCGCGGCTCGC 1194
DB 719 CACGCTCTCTGACCAATCTCTGAGAGACGAAAGGGGCTTCAACAGAGACCTGGG 778
QY 1195 CCGAGCTGATCAGGCTCATGCGCGCGCGCGCATCTCTTCAATGTCACAGGCGCTGC 1254
DB 779 CCTATGTGTAAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 838
QY 1255 AAGAAAGATCTTGTGACAGAGAAAGAGAGCGCGCG 1291
DB 839 AAGAGATCTGATTTGAGAGAGAGAGAGATGAGAGG 875

RESULT 9
LOCUS BT009587 1267 bp mRNA linear PLN 20-JUN-2003
DEFINITION Triticum aestivum clone wreln.pk0049.el:fig, full insert mRNA
sequence.

ACCESSION BT009587
VERSION BT009587.1 GI:32129138
KEYWORDS FLI CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1267)
Tingey,S.V., Woltere,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Haney,C.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA

FEATURES
source location/Qualifiers
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/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wreln.pk0049.el:fig"

ORIGIN

Query Match 24.6%; Score 400.2; DB 8; Length 1267;
Best Local Similarity 66.8%; Pred. No. 2.1e-46;
Matches 586; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

QY 415 AGGCTCAAGATCGGCAACCGCACTGCGCGCGCTGTGAGCGGCGCCATCGCGCGCGC 474
DB 2 AAGATTAAAGTTCGGAAATTCACCTCAAGAGGCTCATCATGTGGGGGATTGACAGCA 61
QY 475 GTGTGAGAGACTTTCGTGCGCGCACTGAGACGATCAGACGCACTGATGTGGGAGC 534
DB 62 GTGTCAAGACAGTTGTGGCGCTTTGAGAGCAATTAGACACATTTGATGTGGCGCAGC 121
QY 535 TCCGCGCGCGACTCCATGCGCGCGGCTTTCCGCTGATCATGCGAGCGAGGGGTGCC 594
DB 122 AATGGGAATTCATCTACGAGAGGTGTTGAC---TCCATCATGAAAGATGAGATGACT 178
QY 595 GGCCTCTTCGCGCGCAACCGCGCTCAAGCTCTCCGCGTGCAGCGCCAGAGGCGCTG 654
DB 179 GGGTGTTCGCGCGCAATTTGGTTATGTCAATTCAGTGCCTCCGCGCAAGCAATCGAG 238
QY 655 CACTTCACCTTACGACACGCGCGAAGATCTGACCCCGAGGCGCGGAGGCGAGCCAG 714
DB 239 CTTTTCCTTTGATGATACGCTAAGAGTTCCTAACCCCAATCTGGGGAAGAGCAAG 298
QY 715 GTTCCCATCCCAACCGCGCTGTGCGCGGAGGCTGCGCGAGTGGCTCAACCTGTGTC 774
DB 299 ATCCCAATCCCTCTCTTCACTAGTGGCAGAGGCTTTTGTGTGCTCACTCACTGTGT 358
QY 775 ACTTATCCCATGAGAGCTGTCAAGACCGCTCTCAACCATGAGAGAGAGGTGTACAGAC 834
DB 359 ACATACCTCTGGAACCTAATTAAGACTCATTAACCATACAGAGAGGTGTATGATTAAC 418
QY 835 CTCCTCAACGCGTTCGTCAGATCTGTCGCGAGAGGCGCGGAGGAGCTGTACCGCGG 894
DB 419 TTCCTCAATGCTTTGTGAAATTTGCTGTGAAGAGGCGCTGTGAGCTGTATGAGGC 478
QY 479 CTGGGCGGAGCTGATGCGCGTGTGTCGCTGACGCGGCGCGCACTTCTACGCTACAG 954
DB 599 ACCTTAAGAGGTGTACAGAAATGTTCAAGACCAATGGAATGCGCAACGTTCCAAC 598
QY 595 AGCGTGGCGGAGTGTACCGCGCGCTGTGGGGAAGAGAGGTGGGAGCGCTCCGAG 1014
DB 539 ACCCTTAAGAGGTGTACAGAAATGTTCAAGACCAATGGAATGCGCAACGTTCCAAC 598
QY 1015 CTGCTGATCGGGTTCGCGCGCGCGCGCATAGCCAGACGCGCTTCCGCTGAGAGG 1074
DB 599 CTGCTCATTTGGGTCTGTGCGAGAGGCTTCAAGACCTGCGCACTTCTCTCAAGGT 658
QY 1075 GCGCGGAGAGATGAGGTGGGCGCGCTGTGGGCGGAGGAGGTGTACAGAACGTGCTG 1134

Db	659	GCTGCAAGCACATGCAGTGGAGACTGTTGGCGCGCCGAAAGTATACAAAGAACATGCTT	718
QY	1135	CACGCCATGTACTGCATCTCTCGAAGAGAGGACCCGCGGCTTACCGGGGCTCGCC	11944
Db	719	CACGCTCTCTCGACCATCTCGAGAGCAAGAGGGGTTGGGGGCTCTTACAGAGACTGGGG	778
QY	1195	CCGAGCTGCATCAAGCTCATGCGCGCGCGCATCTCTTCATGTGCTACGAGGCTGCG	1254
Db	779	CTTACTTGCATGAACTGGTGGCTCTGCTGCTGAGATTTTGTTTATGTGCTTACGAACTTGC	838
QY	1255	AAGAAGATTACTTGTGCACGAGAAAGAGACGGCGCG	1291
Db	839	AAGAAGATTACTGATTGAGAGAGAGAACGATGAACG	875
RESULT 10			
LOCUS	AR438060	449 bp	DNA
DEFINITION	Sequence 15 from patent US 6660850.		linear
ACCESSION	AR438060		
VERSION	AR438060.1	GI:40204511	
KEYWORDS			
SOURCE			
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 449)		
TITLE	Allen, S.M., Lightner, J.E. and Rafalecki, J.A.		
JOURNAL	Nucleic acid encoding a wheat brittle-1 homolog		
FEATURES	Patent: US 6660850-A 15 09-DEC-2003;		
	Location/Qualifiers		
	1..449		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match	24.2%;	Score 392.6;	DB 6; Length 449;
Best Local Similarity	96.4%;	Pred. No. 2.7e-45;	
Matches	432;	Conservative 0;	Mismatches 12; Indels 4; Gaps 3;
QY	1	GGCCAGTGAAGGAGTGAAGACTCTTAAGACATCTTGAAGGAGGACGATCAAGTTCTGCT	60
Db	1	GGCCANTGAGGGAGTGAAGACTCTTAAGAACTCTAGGACGGGCACTATCAAGTTCTGCT	60
QY	61	TGCTTCTCTG -AGATGGCGGGCGGCATGCGCGCGACGACATGTGTGACCAAGACACCG	119
Db	61	TGCTTCTCTGAAAGTAGGGCGGCAGATGGCCGCGACGACATGTGTGACCAAGACACCG	120
QY	120	GGCCTCGCTCGCATGAGCAAGAGAACTGTTATTTGGGCGCGGCTTATTCACGACAGGGCTCGCTT	179
Db	121	GGCCTCGCTCGCATGAGCAAGAGAACTGTTATTTGGGCGCGGCTTATTCACGACAGGGCTCGCTT	180
QY	180	CCCTTGAAGCTGCGACGCCGAGTCCAGAGACTTGAACCTTCCACGACAGGGCTCTGTTGCG	239
Db	181	CCCTTGAAGCTGCGACGCCGAGTCCAGAGACTTGAACCTTCCACGACAGGGCTCTGTTGCG	240
QY	240	CAGCGTGGAGCTCAAGCTGTCTCCACGCGCGCCCGCGGTAGCGCGCGACGATGACGGGAA	299
Db	241	CAGCGTGGAGCTCAAGCTGTCTCCACGCGCGCCCGCGGTAGCGCGCGACGATGACGGGAA	300
QY	300	GGCTGCGCGCGCGCGACGAGTGCACAC -AGCTGCGAGCGCGGGCGAGGCGGGCGTCC	358
Db	301	GGCTGCGCGCGCGCGACGAGTGCACACCACTGACATCGCGGGGCGAGGGGCGTCC	360
QY	359	AGAAAGCCACGAGAGCGAAAAAGCGCAAAAAGCAGACAGCTGAGTCTGA --GGAGGTGAG	416
Db	361	AGAAAGCCACGAGAGCGAAAAAGCGCAAAAAGCAGACAGCTGAGTCTGAAGAGAGGTGAG	420
QY	417	GGTCAAGATCGGCAACCCGCACTGCGG	444
Db	421	GGTCAAGATCGGCAACCCGCACTGCGG	448
RESULT 11			

LOCUS	LOCUS004045	102230 bp	DNA	linear	PLN 15-APR-2004
DEFINITION	Oryza sativa (japonica cultivar-group)	genomic DNA,	chromosome 2,		
ACCESSION	AP004045				
VERSION	AP004045.3	GI:4639078			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
	<p>1 Sasaki, T., Matsumoto, T. and Yamamoto, K. Oryza sativa nipponbare (G3) genomic DNA, chromosome 2, BAC clone: OJ1135_F06 Published Only in Database (2001) 2 (bases 1 to 102230) Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission Submitted (15-ANG-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/ Tel: 81-298-38-7441, Fax: 81-298-38-7468) On Apr 14, 2004 this sequence version replaced g1:38347815. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mlt.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMarkV1), glimmerM (http://www.tigr.org/cdb/glimmerx/glmr form.html), RiceHMM (http://biinformatics.iastate.edu/cgi-bin/sp.cgi), slm4 (http://globin.cse.psu.edu/html/doc/stm4.html), gap2 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRISP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from -21M3 to M3rev of the BAC clone. This sequence of OJ1135_F06 clone has an overlap with P0419409 (DDBJ: AP004869) clone at 5' end and with P054H11 (DDBJ: AP005008) clone at 3' end. The sequence was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/Genomeseg.html.</p>				
	<p>Location/Qualifiers 1..102230 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="genomic DNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="2" /clone="OJ1135_F06" /complement(11735..21686) /gene="OJ1135_F06.1" complement(117235..21686) /gene="OJ1135_F06.1"</p>				
	<p>FEATURES source</p>				
	<p>gene misc_feature</p>				

Db	27673	CGCCGACGTCGGGCCCGGCGCGGAGCGTCGTCATCGGATCGGCGGGGCCATCGCCAG	27733
Qy	1050	CACGGCCACGTTCCCGCTGAGAGTGCGCGCGGAGCAGATCAGGTGGCGCGTCGGCGG	1109
Db	27733	CACGGCCACCTTCCCGCTCAGAGGTGCGCGCGGAGCAGATCAGGTGGCGCGTCGGCGG	27792
Qy	1110	GAGCAGAGTGATCAAGAACGTGCTGCAGCGCATGTACTGTCATCCTCGAGAGAGGCGAC	1169
Db	27793	CGGCGAGGTGATCCGCGCACGTCCTCAACGCGCATGTATGTCATCCTCGCGCGACAGGGCCG	27852
Qy	1170	CGCGGGGCTACACGCGGGGCTCGGCGCCAGGTGATCAACTATCGCGCGCGCGCAT	1229
Db	27853	CGCGGGGCTCTACCGCGGGCTCGGCGCCAGCTGATTAACCTCATGCGCGCGCGCGCAT	27912
Qy	1230	CTCCTTCATGTGCTACGAGGCTCTGACAGAAAGATCTGTGACGAGAAAG	1279
Db	27913	CTCCTTCATGTGCTACGAGGCTCTGACAGAAAGATCTGTGACGAGAAAG	27962

RESULT 12	AP004873/c	138289 bp	DNA	linear	HTG 31-MAY-2002
LOCUS	AP004873				
DEFINITION	<i>Oryza sativa</i> (japonica cultivar-group) *** SEQUENCING IN PROGRESS ***.			chromosome 2 clone P0453G09.	
ACCESSION	AP004873				
VERSION	AP004873.2	GI:21280398			
KEYWORDS	HTG, HTGS, PHASE2.				
SOURCE	<i>Oryza sativa</i> (japonica cultivar-group)				
ORGANISM	<i>Oryza sativa</i> (japonica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS JOURNAL
1 Sasaki, T., Matsumoto, T. and Yamamoto, K. <i>Oryza sativa</i> nipponbare(GA3) genomic DNA, chromosome 2, PAC clone, P0453609 Published only in Database (2002) 2 (Bases 1 to 138289) Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission Submitted (20-MAR-2002) Takuji Sasaki, National Institute of

JOURNAL
Submitted (20-MAR-2002) Takuji Saeki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsaeki@niias.affrc.go.jp, URL: <http://rgp.dna.affrc.go.jp/>,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT
On May 30, 2002 this sequence version replaced gi:19698293.
NOTE: It currently consists of 1 contig. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* **NOTE:** This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

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VERSION	AP004869				
KEYWORDS	AP004869.3	GI:46390373			
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ORGANISM					
	Oryza sativa (japonica cultivar-group)				
	Oryza sativa (japonica cultivar-group)				
	Eurytota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Ehharctoideae; Oryzaceae; Oryza.				
REFERENCE					
AUTHORS	1 Sasaki, T., Matsumoto, T. and Yamamoto, K.				
TITLE	Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 2, PAC				
	clone:PO419A09				
JOURNAL	Published Only in Database (2002)				
REFERENCE	2 (bases 1 to 168064)				
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-MAR-2002) Takuji Sasaki, National Institute of				

COMMENT

On Apr 14, 2004 this sequence version replaced gi:19725615. Genes were predicted from the integrated results of the following: GENSCAN (<http://CCR-081.mtc.edu/GENSCAN.html>), FGENESH (<http://www.softberry.com/>), GeneMark.hmm (<http://opal.biology.gatech.edu/GeneMark/>), GlimmerM (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHM (<http://isp.dna.affrc.go.jp/RiceHM/>), SplicePredictor (<http://bioinformatics.lasate.edu/cgi-bin/wp.cgi>), ssm4 (<http://globin.cse.psu.edu/html/docs/ssm4.html>), gapp2 (<http://www.tigr.org/software/glimmer/>). BLASTN and BLASTX. The genomic sequence was searched against NCBI Nonredundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database, nt (<ftp://ncbi.nlm.nih.gov/blast/db>). Protein homologs of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RCP clone ID.

Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to RGSF standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0419A09 clone has an overlap with P0026H03 (DDBJ: AP004812) clone at 5' end and with OJ113_F06 (DDBJ: AP004865) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rsgp.dna.affrc.go.jp/genomeseq.html>.

FEATURES

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TITLE
JOURNAL
REFERENCE
AUTHORS

Arabidopsis cDNA clones
Unpublished
2 (bases 1 to 1179)
Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L.,
Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Lam,B., Lee,J.M., Lin,J., Miranda,M., Natsusaka,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C.,
Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K.,
Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A.,
and Ecker,J.R.
Direct Submission
Submitted (14-JAN-2002) Salk Institute Genomic Analysis Laboratory
(stgna), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA') : Seki,M., Natsusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

COMMENT

The Salk, Stanford, PEGC (SSP) Consortium members carried out the
sequencing and annotation of the RAPL cDNAs: Cheuk,R., Chen,H.,
Kim,C.J., Meyers,M.C., Shih,P., Banh,J., Bowser,L., Dale,J.M.,
Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B.,
Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S.,
Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C.,
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FEATURES

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 1 (bases 1 to 1334)
 Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N.,
 Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
 Full-length messenger RNA sequences greatly improve genome
 annotation
 JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)

MEDLINE 22088475
 PUBMED 12093376
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 AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 TITLE Full-length cDNA from Arabidopsis thaliana
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1334)
 AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
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